GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2005, 22:15:12.; Search time 5992.54 Seconds
(without alignments)
10576.393 Million cell updates/sec

Title: US-10-632-436A-1
Perfect score: 1308
Sequence: 1 gtacacatataccaacata.........ttaaaaagggttacttagat 1308

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
    1: gb_ba:*
    2: gb_htg:*
    3: gb_in:*
    4: gb_om:*
    5: gb_ov:*
    6: gb_pat:*
    7: gb_ph:*
    8: gb_pl:*
    9: gb_pr:*
   10: gb_ro:*
   11: gb_sts:*
   12: gb_sy:*
   13: gb_un:*
   14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1308	100.0	103157	8	AC011810	Arabidops
2	1295.8	99.1	1312	8	AY063855	Arabidops
3	1264	96.6	1276	8	AB013886	Arabidops
4	1255	95.9	1281	6	AR439833	Sequence
5	1066	81.5	1066	8	AY091291	Arabidops
6	1035	79.1	1035	6	AX507621	Sequence
7	517.8	39.6	1002	8	ATH441073	Arabidops
8	517.8	39.6	1242	8	AY087951	Arabidops
9	517.8	39.6	77483	8	AB028607	Arabidops
10	393.2	30.1	1279	8	AY056169	Arabidops
11	391.2	29.9	1376	8	AY091069	Arabidops
12	391.2	29.9	102540	8	AC079281	Arabidops
13	389.2	29.8	1117	8	AY122941	Arabidops
c 14	379.4	29.0	96808	8	AC011914	Arabidops
15	379.4	29.0	100515	8	AC011665	Arabidops
16	378.4	28.9	1311	8	AY085908	Arabidops
17	378.4	28.9	1315	8	AB013887	Arabidops
18	378.4	28.9	1330	8	AF360312	Arabidops
19	374.6	28.6	1113	8	AF003101	Arabidops
20	369.8	28.3	1090	8	AY056361	Arabidops
21	368	28.1	1059	6	AX507121	Sequence
22	368	28.1	1059	6	AX651568	Sequence
c 23	212.6	16.3	170226	8	AP003450	Oryza sat
24	209.2	16.0	1470	8	BT009310	Triticum
25	190.4	14.5	1098	6	AX660402	Sequence
26	189.8	14.5	1098	6	AX654175	Sequence
27	189.8	14.5	1098	6	AK660052	Oryza sat
28	189.8	14.5	1512	8	AK065008	Oryza sat
29	189.8	14.5	141862	8	AP002913	Oryza sat
30	183.2	14.0	930	6	AX654438	Oryza sat
31	178.2	13.6	141715	8	AC130725	Oryza sat
32	178.2	13.6	167557	8	AC136492	Oryza sat
33	178.2	13.6	177861	8	AC135925	Oryza sat
34	152.4	11.7	274	11	AL823960	Arabidops
35	140	10.7	1126	8	AY085197	Arabidops
36	140	10.7	1389	8	AK117646	Arabidops
37	140	10.7	142001	8	AL138642	Arabidops
38	132.2	10.1	477	6	AX505488	Sequence
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c 41	132.2	10.1	31733	8	AC007135	Arabidops
42	132.2	10.1	120938	8	AC007017	Arabidops
43	132	10.1	933	6	AX589947	Sequence
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45	132	10.1	1370	8	AK118045	Arabidops

ALIGNMENTS

RESULT 1
AC011810
LOCUS   AC011810   103157 bp   DNA   linear   PLN 01-SEP-2000
DEFINITION Arabidopsis thaliana chromosome I BAC T6J4 genomic sequence,
            complete sequence.
ACCESSION   AC011810
VERSION   AC011810.8 GI:8576186
KEYWORDS   HTG.
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 103157)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S.,
            Buehler,E., Chao,Q., Chin,C., Chiou,J., Choi,E., Gonzalez,A.,
            Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M.,
            Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H.,
            Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A.
            and Davis,R.W.
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 103157)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E.,
            Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C.,
            Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,
            Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P.,
            Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J.,
            Theologis,A. and Davis,R.W.
  TITLE   Direct Submission
  JOURNAL   Submitted (15-OCT-1999) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
REFERENCE   3 (bases 1 to 103157)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E.,
            Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C.,
            Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,
            Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P.,
            Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J.,
            Theologis,A. and Davis,R.W.

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TITLE     Direct Submission
JOURNAL   Submitted (01-JUN-2000) DNA Sequencing and Technology Center,
          Stanford University, 855 California Avenue, Palo Alto, CA 94304,
          USA
REFERENCE 4  (bases 1 to 103157)
AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
          Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
          and Davis,R.W.
TITLE     Direct Submission
JOURNAL   Submitted (21-JUN-2000) DNA Sequencing and Technology Center,
          Stanford University, 855 California Avenue, Palo Alto, CA 94304,
          USA
REFERENCE 5  (bases 1 to 103157)
AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
          Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
          and Davis,R.W.
TITLE     Direct Submission
JOURNAL   Submitted (01-SEP-2000) DNA Sequencing and Technology Center,
          Stanford University, 855 California Avenue, Palo Alto, CA 94304,
          USA
COMMENT   On Jun 21, 2000 this sequence version replaced gi:8050909.
          Bases 1-5,179 of clone T6J4 overlap with bases 94,580-99,758 of IGF
          BAC clone F3F19 (gb|AC007357).
          e-mail for correspondence: arab@sequence.stanford.edu  Genes with
          similarity to proteins in the databases are named 'putative',
          '-like' or 'similar to'. Genes that have EST similarity but no
          significant protein similarity are described as 'unknown proteins'.
          Genes that are annotated based only on gene prediction software
          are described as 'hypothetical proteins'.  The gene prediction
          programs used to predict genes include: Grail (Informatics Group,
          Oak Ridge National Laboratory,
          http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
          http://genes.mit.edu/GENSCAN), FEXA (Victor Solovyev,
          http://genomic.sanger.ac.uk/gf/gf.shtml), and NetPlantGene (S.M.
          Hebsgaard, et al., CBS, Technical University of
          Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
FEATURES            Location/Qualifiers
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                     /cultivar="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="I"
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                     F3F19 (gb|AC007357). See GenBank record for BAC F3F19 for
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Query Match     100.0%;    Score 1308;    DB 8;    Length 1031157;
Best Local Similarity   100.0%;    Pred. No. 5.8e-277;
Matches 1308;    Conservative  0;    Mismatches  0;    Indels  0;    Gaps  0;

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Qy      121 TACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 180
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Qy      181 AGGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCGT 240
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Qy      241 AGAAGCTGAATCTAGGAGAAGCTTCCGTCGTCGTCAAAATACAAGGTGTGGTGCCACAACCAAA 300
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Qy      301 CGGAAGATGGGGAGCTCAGATTACGAGAAACACCAGCGCGTGTGCTCCGGGACATTCAA 360
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Qy      481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAAACGAAGAGTTAGA 540
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Qy      661 AGCGGTAACGGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGAAACATCACGC 720
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RESULT 2
AY063855
LOCUS       AY063855                1312 bp    mRNA    linear    PLN 18-SEP-2002
DEFINITION  Arabidopsis thaliana putative DNA-binding protein RAV1 (At1g13260)
            mRNA, complete cds.
ACCESSION   AY063855
VERSION     AY063855.1    GI:17380761
KEYWORDS    FLI cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 1312)
AUTHORS     Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
            Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C.,
            Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
            Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
            Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
            Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
            Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
            Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE       Arabidopsis Full Length cDNA Clones
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1312)
AUTHORS     Yamada,K., Banh,J., Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D.,
            Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C.,
            Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H.,
            Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A.,
            Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J.,
            Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
            Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
            Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE       Direct Submission
JOURNAL     Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
```

Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J.,
Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M.,
Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C.,
Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T.,
Karlin-Neuman,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C.,
Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki.M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.

FEATURES   Location/Qualifiers
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                     /ecotype="Columbia"
                     /note="This clone is in a modified pBluescript vector
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ORIGIN

Query Match   99.1%;   Score 1295.8;   DB 8;   Length 1312;
Best Local Similarity   99.8%;   Pred. No. 2.1e-274;
Matches 1297; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy     9 ATACCAACACATAATTCACAACAACAACAAAACACATTCTGTTTTCTCCCATTGTTTCAAA   68
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Db     1 ATACCAACACATAATTCACAACAACAACAACACATTCTGTTTTCTCCCATTGTTTCAAA    60

Qy    69 CCATAAAAAAAAAAACACAGATTAAATGAATGAGTAGCGTTGATGAGAGTACTACAAGTA  128
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Db    61 CCATAAAAAAAAAAACATAGATTAAATGAATGAGTAGCGTTGATGAGAGTACTACAAGTA  120

Qy   129 CAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACT  188
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Db   121 CAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACT  180

Qy   189 TATACAGGATGGGAAGCGGATCAAGCCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTG 248
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Db   181 TATACAGGATGGGAAGCGGATCAAGCCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTG 240

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Qy   309 GGGGAGCTCAGATTTACAGAGAAACACCAGCGCGTGTGGCTCGGACATTCAACGAAGAAG  368
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Db   481 AATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTA 540

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Qy   609 ATGATGGTGTTTTCTACGACGGGGGTTTAGTCGGCGGAGGCACTGTTGTTGAGAAAGCGGTAA 668
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Qy   729 ATTTTCCGTACCGTCAAGTAACGTTCCGTAAGGAGGTGTTGTGAACTTTGAGGACG 788
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Qy   789 TTAACGGAAAGTGTGGAAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTT 848
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Qy   909 GTTTCAGTAGATCTCAACGTCAGATCAACAGTGTACATTGGGGTGGAAGTCGAGATCCG 968
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Db   901 GTTTCAGTAGATCTCAACGTCAGATCAACAGTGTACATTGGGGTGGAAGTCGAGATCCG 960

Qy   969 GGTCAGATTTAGATGCGGGTCGGGTTTGGGTTTGGGAGTTAACATTTCACCGGAGA 1028
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Qy  1029 GTTCAAGAACGACGTCGTAGGAGAACAAAAGAGTGAACAAAAGAGTGAACGATACTGAGATGTATCGTTGG 1088
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Qy  1089 TGTGTAGCAAGAAGCAACGACCATCTTCAGCGCCTGTAACAACTCTTCTTCTTTTTTT 1148
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Qy  1149 CTTTTTGTTGTTGTTTAATAATTTTTAAAAACTTCCATTTTCGTTTTCTTATTTGCATCGGTT 1208
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Db  1141 CTTTTTGTTGTTGTTTAATAATTTTTAAAAACTTCCATTTTCGTTTTCTTATTTGCATCGGTT 1200

Qy  1209 TCTTTCTTCTTGTTCTTTACCAAAGGTTCATGAGTTGTTTTTGTTTTTTGTATTGATGAACTGTAAA 1268
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Db  1201 TCTTTCTTCTTGTTCTTTACCAAAGGTTCATGAGTTGTTTTTGTTTTTTGTATTGATGAACTGTAAA 1260

Qy  1269 TTTTATTTATAGGATAAAATTTAAAAAGGGTTACTTAGA 1307
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RESULT 3
AB013886
LOCUS   AB013886   1276 bp   mRNA   linear   PLN 06-FEB-1999
DEFINITION Arabidopsis thaliana mRNA for RAV1, complete cds.
ACCESSION   AB013886
VERSION   AB013886.1 GI:3868856
KEYWORDS   RAV1.
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (sites)
  AUTHORS   Kagaya,Y., Ohmiya,K. and Hattori,T.
  TITLE   RAV1, a novel DNA-binding protein, binds to bipartite recognition
            sequence through two distinct DNA-binding domains uniquely found in
            higher plants
  JOURNAL   Nucleic Acids Res. 27 (2), 470-478 (1999)
   MEDLINE   99081843
   PUBMED   9862967
REFERENCE   2 (bases 1 to 1276)
  AUTHORS   Hattori,T. and Kagaya,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-MAY-1998) Tsukaho Hattori, Mie University, Center for
            Molecular Biology and Genetics; 1515 Kamihama-cho, Tsu, Mie
            514-8507, Japan (E-mail:hattori@gene.recs.mie-u.ac.jp,
            Tel:81-592-231-9074, Fax:81-592-231-9048)
FEATURES   Location/Qualifiers
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ORIGIN
Query Match   96.6%; Score 1264; DB 8; Length 1276;
Best Local Similarity 99.9%; Pred. No. 2.1e-267;
Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 1;

Qy   334 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGACGAGAGCCCGCTCGTTCGCCTACGACGT 393
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Db   301 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGACGAGAGCCCGCTCGTTCGCCTACGACGT 360

Qy   394 CGCGGTTCACAGGTTCCGTCGCCGTGACGCGTCACAAATTCAAAGACGTGAAGATGGA 453
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Db   361 CGCGGTTCACAGGTTCCGTCGCCGTGACGCGTCACAAATTCAAAGACGTGAAGATGGA 420

Qy   454 CGAAGACGAGGTCGATTTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAG 513
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Db   421 CGAAGACGAGGTCGATTTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAG 480

Qy   514 GAAACATACTTATACAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGTAACGGAAA 573
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Qy   574 CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACGGGGTT 633
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Db   541 CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACGGGGTT 600

Qy   634 TAGATACGGCGGGAGCGACTCGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAA 693
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Db   601 TAGATACGGCGGGAGCGACTCGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAA 660

Qy   694 CCGTTTGGTTATACCGGAAACATCAGCGAGAGAAACATTTCCGTTACCGTCAAGTAACGT 753
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Db   661 CCGTTTGGTTATACCGGAAACATCAGCGAGAGAAACATTTCCGTTACCGTCAAGTAACGT 720

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Qy   814 TTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGGTTCGT 873
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Qy   934 TCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGCGGGT 993
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Qy   994 TTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTAGGAAA 1053
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Db   961 TTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTAGGAAA 1020

Qy   1054 CAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGCAATCTT 1113
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Qy   1114 TCACGGCCTCGTAACAACTCTTCTT-CTTTTTTTTTTTCTTTTTGTTTTTTAATAATTTTA 1172
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Db   1081 TCACGGCCTCGTAACAACTCTTCTTTCTTTTTTTTTTTCTTTTTGTTTTTTAATAATTTTA 1140

Qy   1173 AAAACTCCATTTCGTTTTCGTTTTGCATCGGTTTCTTCTTCTTGTTTTACCCAAAGGT 1232
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Qy   1233 TCATGAGTTGTTTTTGTGTTATTGATGAACTGTAAATTTATTTATTTAGGATAAATTTTAA 1292
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Db   1201 TCATGAGTTGTTTTTGTGTTATTGATGAACTGTAAATTTATTTATTTAGGATAAATTTTAA 1260

Qy   1293 AAAGGGTTACTTAGAT 1308
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Db   1261 AAAGGGTTACTTAGAT 1276

RESULT 4
AR439833
LOCUS   AR439833   1281 bp   DNA   linear   PAT 20-FEB-2004

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DEFINITION   Sequence 65 from patent US 6664446.
ACCESSION    AR439833
VERSION      AR439833.1  GI:42665798
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 1281)
  AUTHORS    Heard,J., Broun,P., Riechmann,J.L., Keddie,J., Pineda,O., Adam,L.,
             Samaha,R., Zhang,J., Yu,G.-L., Ratcliffe,O., Pilgrim,M.,
             Jiang,C.-Z. and Reuber,L.
  TITLE      Transgenic plants comprising polynucleotides encoding transcription
             factors that confer disease tolerance
  JOURNAL    Patent: US 6664446-A 65 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1..1281
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                     /mol_type="genomic DNA"
ORIGIN

Query Match             95.9%;  Score 1255;  DB 6;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 2e-265;
Matches 1266;  Conservative     0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy      29 CACAACACAAACACATTCTGTTTCTCCATTCGTTTCAAACCATAAAAAAAAAACACAGAT   88
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Db       1 CACAACACAAACACATTCTGTTTCTCCATTCGTTTCAAACCATAAAAAAAAAACACAGAT   60

Qy      89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC  148
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Db      61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC  120

Qy     149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGTAGTAGTAACTTATACAGGATGGGAAGCGGA  208
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Db     121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGTAGTAGTAACTTATACAGGATGGGAAGCGGA  180

Qy     209 TCAAGCGGTTGTGTTGAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  268
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Db     181 TCAAGCGGTTGTGTTGAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  240

Qy     269 TCAAAATACAAAGGTGTGGTGCCACAACCGAAGATGGGAGCTCAGATTTACGGAG  328
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Db     241 TCAAAATACAAAGGTGTGGTGCCACAACCGAAGATGGGAGCTCAGATTTACGGAG  300

Qy     329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC  388
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Db     301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC  360

Qy     389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCGGTCACAAATTTCAAAGACGTGAAG  448
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Db     421 ATGGACGAAGACGAGGCCGATTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATG  480

Qy     509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC  568
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Db     481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC  540

Qy     569 GGAAACATGACTAGGACGGTTGTTAACGTCGGGGTTGAGTAATGATGGTTTTCACGACG  628
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Db     541 GGAAACATGACTAGGACGGTTGTTAACGTCGGGGTTGAGTAATGATGGTTTTCACGACG  600

Qy     629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCCGGTTAACGCCAAGCGGTTGGGAAG  688
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Db     601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCCGGTTAACGCCAAGCGGTTGGGAAG  660

Qy     689 CTAAACCGTTGTTATACCGAGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT  748
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Db     661 CTAAACCGTTGTTATACCGAGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT  720

Qy     749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  808
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Db     721 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  780

Qy     809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG  868
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Db     781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG  840

Qy     869 TTCGTTAAGGAGAAGAATCTACGTGCTCGGTGACGTGGTGAGTTTCAGTAGATCTAACGT  928
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Db     841 TTCGTTAAGGAGAAGAATCTACGTGCTCGGTGACGTGGTGAGTTTCAGTAGATCTAACGGT  900

Qy     929 CAGGATCAACAGTTGTACATTGGGGTGGAGTCGGAGCTCGAGATCCGGTCAGATTAGATGCGGGT  988
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Db     901 CAGGATCAACAGTTGTACATTGGGGTGGAGTCGGAGCTCGAGATCCGGTCAGATTAGATGCGGGT  960

Qy     989 CGGGTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA  1048
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Db     961 CGGGTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA  1020

Qy    1049 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC  1108
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Db    1021 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC  1080

Qy    1109 ATCTTTCACGCGCCTCGTAACAACTCTCTTCTTTTTTTTCTTTTGTGTTTTGTTTTAAATAATT  1168
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Db    1081 ATCTTTCACGCGCCTCGTAACAACTCTCTTC-TTTTTTTTCTTTTGTGTTTTGTTTTAAATAATT  1139

Qy    1169 TTTAAAAACTCCATTTTCGTTTTCGTTTTCGTTTTCTTTATTTGCATCGGTTCTTCTTCGTTGTTTACCAA  1228
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Db    1140 TTTAAAAACTCCATTTTCGTTTTCGTTTTCGTTTTCTTTATTTGCATCGGTTCTTCTTCGTTGTTTACCAA  1199

Qy    1229 AGGTTCATGAGTTGTTTTTGTTGTATTGATGAACTGTAAATTTTATTTTATTAGGATAAAATT  1288
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Qy    1289 TTAAAAA  1295
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Db    1260 TTAAAAA  1266
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RESULT 5
AY091291
LOCUS       AY091291                1066 bp    mRNA     linear   PLN 18-SEP-2002
DEFINITION  Arabidopsis thaliana putative DNA-binding protein RAV1 (At1g13260)
            mRNA, complete cds.
ACCESSION   AY091291
VERSION     AY091291.1  GI:20259028
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1066)
  AUTHORS   Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
            Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
            Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
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            Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
            Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE     Arabidopsis Open Reading Frame (ORF) Clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1066)
  AUTHORS   Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
            Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
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Qy   332 CACCAGCGGCTGTGCTCGGGACATTCAACGAAGAAGACGAAGCGCTCGTGCCTACGAC 391
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Db   301 GTCGCGGTTCACAGTTCCGTCGCCCGTGACGCGCCGTCACAAATTCAAAGACGTGAAGATG 360

Qy   452 GACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAAATCTGAGATCGTTGATATGTTG 511
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Qy   692 AACCGTTGTTATACCGAAACATCACGAGAAACATTTCCGTACCGTCAAGTAAC 751
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Qy   752 GTTTCCGTGAAAGGAGTGTTGTTGAACTTGAGGACGTTAACGCGGAAAGTGTGGAGGTTC 811
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Db   661 GTTTCCGTGAAAGGAGTGTTGTTGAACTTGAGGACGTTAACGCGGAAAGTGTGGAGGTTC 720

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Db   781 GTTAAGGAGAAGAATCTACGTGGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAG 840

Qy   932 GATCAACAGTTGTACATTGGGTGGAAGTCCGGGTCAGATTTAGATGCGGGTCGG 991
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Qy   992 GTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTAGGA 1051
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Qy  1052 AACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGGTGAGGAGCAAGGCCATC 1111
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Db   961 AACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGGTGAGGAGCAAGAACGCCATC 1020

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TITLE   Direct Submission
JOURNAL   Submitted (20-MAR-2002) Plant Gene Expression Center, 800 Buchanan
          Street, Albany, CA 94710, USA
COMMENT   The RIKEN Genomic Sciences Center (GSC) members carried out the
          collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
          Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
          Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
          Hayashizaki,Y. and Shinozaki,K.
          The Salk, Stanford, PGEC (SSP) Consortium members constructed and
          sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K.,
          Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,
          Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
          Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,
          Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,
          Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,
          Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
          Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
          to this work. Shinozaki.K. (RIKEN GSC) and Theologis,A. (SSP
          /PGEC) contributed equally to this work as PIs.
          Annotation is based on the January 2002 version of the Arabidopsis
          genome submitted to GenBank.
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                     /note="This clone is in pUNI 51."
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                     /gene="At1g13260"
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                     /codon_start=1
                     /evidence=experimental
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                     NMTRTLITSGLSNDGVSTGFRSAEALFEKAVTPSDVGKLNRIVIPKHHAEKHFPLPS
                     SNVSVKGVLLNFEDVNGKVWRFRYSYWNSSQSVVLTKGWSRFVKENLRAGDVVSFSR
                     SNGQDDQLYIGWKSRSGSDLDAGRVLRLFGVNISPESSRNDVVGNKRVNDTEMLSLVC
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     3'UTR   1036..1066
                     /gene="At1g13260"
ORIGIN

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Matches 1066; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   92 ATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGTTCCATCGTGAAACCCCG 151
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Db    1 ATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGTTCCATCGTGAAACCCCG 60

Qy  152 GCGATAACTCCCGGCGAAAAAGTCGTCGGAGTAACTTATACAGGATGGGAAGCCGGATCA 211
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Db   61 GCGATAACTCCCGGCGAAAAAGTCGTCGGAGTAACTTATACAGGATGGGAAGCCGGATCA 120

Qy  212 AGCGGTTGTGTTAGATTCAGAGAACGACGGCGTAGAAGTGAATCTAGGAAGCTTCCGTCGTCA 271
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Db  121 AGCGGTTGTGTTAGATTCAGAGAACGACGGCGTAGAAGTGAATCTAGGAAGCTTCCGTCGTCA 180

Qy  272 AAATACAAAGGTGTGTGCCACCAACAAACGGAAGAGATGGGGAGCTCAGATTTACCAGAGAAA 331
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RESULT 6
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LOCUS   AX507621   1035 bp   DNA   linear   PAT 27-SEP-2002
DEFINITION Sequence 2316 from Patent WO0216655.
ACCESSION   AX507621
VERSION   AX507621.1 GI:23388858
KEYWORDS   .
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
  TITLE   Stress-regulated genes of plants, transgenic plants containing
            same, and methods of use

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JOURNAL    Patent: WO 0216655-A 2316 28-FEB-2002;
           The Scripps Research Institute (US) ; Syngenta Participations AG
           (CH)
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ORIGIN

Query Match             79.1%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity 100.0%;  Pred. No. 4.7e-217;
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Qy        152 GCGATAACTCCGCGCGAAAAAGTCGTCTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA 211
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Qy        452 GACGAAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAAATCTGAGATCGTTGATATGTTG 511
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Qy        752 GTTTCCGTGAAAGGAGTGTTGTTGAACTTGTTGAACGTTAACGGAGAAGTGTGGAGGTTC 811
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Qy        812 CGTTACTCGTATTGGAACAGTAGTCAGAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGGTTC 871
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Db        781 GTTAAGGAAGAATCTACGTGCGTGACGTCGTGACTGTTAGTTCAGTAGGATCTCACGGTCAG 840

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RESULT 7
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LOCUS       ATH441073               1002 bp    mRNA    linear   PLN 15-APR-2002
DEFINITION  Arabidopsis thaliana mRNA for putative auxin response factor 14
            (arf14 gene).
ACCESSION   AJ441073
VERSION     AJ441073.1  GI:20152523
KEYWORDS    arf14 gene; auxin response factor 14.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Carabelli,M., Ciarbelli,A.R., Ruzza,V., Sessa,G., Steindler,C. and
            Ruberti,I.
  TITLE     Nucleotide sequence of the putative Arabidopsis ARF14
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1002)
  AUTHORS   Ruzza,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-APR-2002) Ruzza V., Centro di studio per gli Acidi
            Nucleici, Consiglio Nazionale delle Ricerche, c/o Dip. Genetica e
            Biologia Molecolare, Universita La Sapienza, P.le Aldo Moro 5,
            00185 Rome, ITALY
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ORIGIN

Query Match             39.6%;  Score 517.8;  DB 8;  Length 1002;
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REFERENCE   1 (bases 1 to 1242)
AUTHORS   Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
            Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE   Full-length messenger RNA sequences greatly improve genome
            annotation
JOURNAL   Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE   22208475
PUBMED   12093376
REFERENCE   2 (bases 1 to 1242)
AUTHORS   Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
            Feldmann,K.
TITLE   Full-length cDNA from Arabidopsis thaliana
JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 1242)
AUTHORS   Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
            Feldmann,K.
TITLE   Direct Submission
JOURNAL   Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
            Malibu, CA 90265, USA
COMMENT   This clone sequence is one of 5,000 Ceres full-length cDNAs made
            available to TIGR and Genbank. The following quality assessment of
            this set was done by comparison with known proteins: two percent of
            the clones are estimated to be 5'-truncated; less than one percent
            are 3'-truncated; approximately two percent represent alternative
            splice variants, including unspliced introns and spliced exons; one
            percent may contain premature stop codons; five percent may have
            frame shifts in a coding region. A sequence is considered to be
            5'-truncated if it lacks the translation initiation start (ATG). A
            sequence is considered to be 3'-truncated if it lacks the
            C-terminal end of the encoded protein. Please note that these cDNA
            sequences are derived from the Ws or Laer ecotypes and therefore
            may contain polymorphisms when compared to sequences from Col-0.
            Genset carried out the library production and sequencing of the
            full-length clones. Ceres, Inc. carried out the clustering of the
            5' sequences, selection of clones, and sequence assembly.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /clone="39877"
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                     /db_xref="GI:21593532"
                     /translation="MDAMSSVDESSTTTDSIPARKSSSPASLLYRMGSGTSVVLDSEN
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                     ETTAPALASMVVMTGFKTAELLFEKTVIPSDVGKLNRLVIPKHQAEKHFPLPLGNNNV
                     SVKGMLLNFEDVNGKVWRPRYSYWNSSQSYVLTKGWSRFVKEKRLCAGDLISFKRSND
                     QDQKFFIGWKSKSGLDLETGRVMRLFGVDISLNAVVVVKETTEVLMSSLRCKNQRVL"
ORIGIN

Query Match   39.6%; Score 517.8; DB 8; Length 1242;
Best Local Similarity 76.6%; Pred. No. 2.7e-103;
Matches 719; Conservative   0; Mismatches 172; Indels 48; Gaps 5;

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Db     97 GAGTAGCGTAGACGAGAGCTCACAACTACAGATTCCATTCCATTCCGGCGAAAGTCATCGTC 156

Qy    160 TCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGAAGCCGGATCAAGCGTTGT 219
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Db     72 TCCGGGCGA------------GTTTACTATATAGAATGGAAGCCGGAACAAGCGTGGT 116

Qy    220 GTTAGATTCAGAGAACGGCGTA---------GAAGCTGAATCTAGAGAGCCTTCCGTC 267
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Db    117 ACTTGATTCAGAGAAGACAAAGCGGTGTCGAAGTCGAAGTCGAATCAAGAAAAGCTTCCTTC 176

Qy    268 GTCAAAATACAAAGGTGGTGGTGCCACAACCAAACCGAGAGATGGGAGCTCAGATTTACGA 327
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Db    177 TTCAAGATTCAAAGGTGTTGTTCCTCAACCAAATGGAAGCCGGAGCTCAGATTTACGA 236

Qy    328 GAAACACCAGCGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTA 387
Db    237 GAAACATCAACGGCGTGTGGCTTGGTACTTTCAACGAAGAAGACGAAGCAGCTCGTGCTTA 296

Qy    388 CGACGTCGCGGTTCACAGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAGAGCGTGAA 447
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Qy    448 GATGGACGAAGACGAGGTCGATTTCTTCGAATTCCTCATTCGGAAATCTGAGATCGTTGATAT 507
Db    354 GACGTTCGAAGAAGAGGTTGAGTTCTTAAACGCGCATTCGAAATCGAGAATCAGAGATCGTAGATAT 413

Qy    508 GTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAA 567
Db    414 GTTGAGAAAACACCACTTACAACGAAGAGTTAGACCAAAGAAAGAACGTAACCGTGACGGTAA 473

Qy    568 CGGAAAACATGACTAGGACGGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGAC 627
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Qy    628 GGGGTTAGATCGCGGGAGGCCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAA 687
Db    522 GGGGTTAAAACGCGGCAGTTACTGTTTGAGAAAAACGTAACGCCAAGTGACGTCGGGAA 581

Qy    688 GCTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCA-- 745
Db    582 ACTAAACCGTTAGTTATACCAAAAAACACCAAGCCGGAGAAACATTTTCCGTTACCGTTAGG 641

Qy    746 ----AGTAACGTTTCCGTGAAAGGTATGCGTTTAAAGGTATGCTGTTGAATTTCGAAGACGT 801
Db    642 TAATAATAACGTCGTCCGTTAAAGGTATGTTTGAATTTCGAAGACGTTAACGGGAAAGT 701

Qy    802 GTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTG 861
Db    702 GTGGAGGTTCCGTTACTCTTATTGGAATAGTAGTCAAAGTTATGTTTGTTGACCAAAGGTTG 761

Qy    862 GAGCAGGTTCGTTGAAGGAGAAGAAATCACGTGCTGTCGTGGTTAGTTTCAGTAGATC 921
Db    762 GAGTAGATTCGTTAAAGAGAAGAAGACTTTGTGCTCGTGGTGATTTGATCAGTTTAAAAGATC 821

Qy    922 TAACGGTCAGGATCAACAGTTGTACATTGGGTGGTGAAGTCGAGATCCGGGTCAGATTTAGA 981
Db    822 CAACGATCAAGATCAAGATCAAAAATTCTTTATCGGGTGGAAATCGAAATCCGGGTTGGATCTAGA 881

Qy    982 TGCGGGTCGGGTTTTGAGATTGTTCGGAGTTAACATTTC 1020
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RESULT 8
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LOCUS   AY087951   1242 bp   mRNA   linear   PLN 14-APR-2003
DEFINITION Arabidopsis thaliana clone 39877 mRNA, complete sequence.
ACCESSION   AY087951
VERSION   AY087951.1 GI:21406725
KEYWORDS   FLI cDNA.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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Qy  328 GAAACACCAGCGCGTGCCTCGGGACATTCAACGAAGAAGACGAAGGCCGTCGTGCCTA 387
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Db  322 GAAACATCAAGCGCGTGCGTGGTACTTCAACGAGGAAGAGACGAAGCGAGCAGCTCGTGCCTA 381

Qy  388 CGACGTCGCGGTTCACAGTTCCGTCGCGTGACGCCGTCACAAATTTCAAAGACGTGAA 447
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Db  382 CGACGTCGCGGTTCACCGTTCCCGGCCGGATGCGCCGGTTACTAATTTCAAAGAC---AC 438

Qy  448 GATGGACGAAGACGACGGTCGATTTCTTCATTCGAAATCTGAAATCTGATCGTTGATAT 507
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Db  439 GACGTTCGAAGAAGAGAGGTTGAGTTCTTAAACGGCATTCGAAATCAGAGATCGTAGATAT 498

Qy  508 GTTGAGGAGAACATACTTATAACGAAGAGTGTAGAGCAGAGTAAACGGCGTCGTAATGGTAA 567
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Db  499 GTTGAGAAAACACCACTTACAAAGAGAGAGTAGACCAAAGGAAAACGTAACCGTGACGGTAA 558

Qy  568 CGGAAAACATGACTAGGACGTCGTGTTAACGTCGGGTTGAGTAATGATGTGTTTCTACGAC 627
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Db  559 CGGAAAAGAGACGACGACGGCCGTTGCTTGGCTTCCATG----------GTGGTTATCGAC 606

Qy  628 GGGGTTTAGATCCGGCGGAGGCACTGTTGAGAAAGCCGGTAACGCCAAGCGACGTTGGGAA 687
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Qy  688 GCTAAACCGTTTGGTTATACCGGAAACATCACGCGAGAGAAACATTTTCCGTTACCGTCA-- 745
        |||||||||||| |||||||| | |||| ||  |||| |||||||||||||||||||| ||
Db  667 ACTAAACCGTTTAGTTATACCAAAAACACCAAGCGGAGAAACATTTTCCGTTACCGTTAGG 726

Qy  746 ---AGTAACGTTTCCGTGAAAGAGGAGTGTGTTGAACTTGAGGACGTTAACGGGAAAGT 801
           || |||||| ||||  ||||  || ||||| ||| |||  ||||||||||||||||
Db  727 TAATAATAACGTCTCCGTTTAAAGTATGCGTGTTCGAAATTTCGAGACGTTAACGGGAAAGT 786

Qy  802 GTGGAGGTTCCGTTACTCGTATTGGAACGTCAGAGTTATGTTTGACTAAAGGTTG 861
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Db  787 GTGGAGGTTCCGTTACTCCTTATTGGAATAGTAGTTATGTTTATGTTGACCAAAAGGTTG 846

Qy  862 GAGCAGGTTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATC 921
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Db  847 GAGTAGATTCGTTAAAGAGGAAGAGAGACACTTTGTGCTGGTGGTTGATCAGTTTTAAAAGATC 906

Qy  922 TAACGGTTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAAGTTCGGGTCAGATTTAGA 981
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Db  907 CAACGATCAAGATCAAAAATTCTTTATCCGGTGGAAATCGAAATCCGGGTTGGATCTAGA 966

Qy  982 TGCGGGTCGGGTTTGAGATTGGTTCGGAGTTAACATTTC 1020
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Db  967 GACGGGTCGGGTTATGAGATTGTTTGGGGTGATTATTTC 1005
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COMMENT   Address for correspondence: kaos@kazusa.or.jp
          For the latest information on annotation of this clone, please see
          http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K13N2
          Genes with similarity to proteins in the databases are described in
          'product' or 'note' qualifiers. Genes that have no significant
          protein similarity are described as 'unknown protein'.
          The software programs used to predict genes include: Grail
          (Informatics Group, Oak Ridge National Laboratory,
          http://compbio.ornl.gov/Grail-1.3/),
          GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
          NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
          Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
          SplicePredictor (Volker Brendel, Stanford University,
          http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
          Genes encoding tRNAs are predicted by tRNAscan-SE
          (Sean Eddy, Washington University School of Medicine, St. Louis,
          http://genome.wustl.edu/eddy/tRNAscan-SE/).
          This sequence may not be the entire insert of this clone. It may be
          shorter because we remove overlaps between neighboring submissions.
          The 5' clone is T5M7 and the 3' clone is K9I22.

FEATURES   Location/Qualifiers
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                     MRRGSSFPGDGBIMGKLSAQEVMDAKALAASKSHSRAERRRERINTHLAKLRSILPN
                     TTKTDKASLLAEVIQHMKELKRQTSQITDTYQVPTECDLTVDSSYNDEEGNLVIRAS
                     FCCQDRTDLMHDVINALKSLRLRTLKAEIATVGGRVKNILFLSREYDDEDHDSYRRN
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RESULT 9
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DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K13N2.
ACCESSION   AB028607 BA000014
VERSION   AB028607.1 GI:5041960
KEYWORDS   .
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids II; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS   Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S.
TITLE   Structural analysis of Arabidopsis thaliana chromosome 3. I.
            Sequence features of the regions of 4,504,864 bp covered by sixty
            P1 and TAC clones
JOURNAL   DNA Res. 7 (2), 131-135 (2000)
MEDLINE   20277480
PUBMED   10819329
REFERENCE   2 (bases 1 to 77483)
AUTHORS   Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S.
TITLE   Direct Submission

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CDS   join(34502. .34610,34772. .34805,34885. .35122,35196. .35357,
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KIPSGVPFRVAFLDNIFAVNYHDNKIWCCKTREGSRSWTKIKNQVEDFSDIILHMGR
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Query Match   39.6%;   Score 517.8;   DB 8;   Length 77483;
Best Local Similarity   76.6%;   Pred. No. 3.6e-103;
Matches 719;   Conservative   0;   Mismatches 172;   Indels 48;   Gaps   5;

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Qy   220 GTTAGATTCAGAGAACGGCGTA----------- GAAGCTGAATCTAGGAGAGCTTCCGTC   267
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Qy   388 CGACGTCGCCGTTCACAGGTTCCGTCGCCGGTGACCGGTCACAAATTCAAAGACGTGAA   447
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Db 33497 CGACGTCGCGCGCTCACCGTTTCCGTGGCGCGATGCCGTTACTAATTTCAAAGAC---AC   33553

Qy   448 GATGGACGAAGACGAGGTCGATTTCTGAATTCTCATTCGAAATCTGAAATCGTTGATAT   507
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Db 33554 GACGTTCGAAGAAGAGGTTGAGTTCTTAAACGCGATTCAAACCGCATCAGAGATCGTAGATAT   33613

Qy   508 GTTGAGGAAACATACTTATAACGAAGAGTTAGACGAGTTAGACGAGTAAATGGTAA   567
           |||||||||||| | |||| |||||||||||||||||||||||||||||| |||
Db 33614 GTTGAGAAAACACACTTACAAGAAGAGTTAGACCAAAGGAAACGTAACCGTGACGGTAA   33673

Qy   568 CGGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGAC   627
           ||||||||||||||||||||||||||||||||||||||||||| |
Db 33674 CGGAAAAGAGACGACCGGCGTTTGCTTTGGCTTGGATG----------GTCGGTTATGAC   33721

```
JOURNAL     Submitted (23-SEP-2002) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Yamada,K., Chan,M.M.,
            Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M., Quach,H.L.,
            Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yu,G.,
            Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M.,
            Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W.,
            Ecker,J.R. and Theologis,A.

            Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
            this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
     source          1..1279
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /chromosome="1"
                     /clone="RAFL08-13-K22 (R11283)"
                     /ecotype="Columbia"
                     /note="This clone is in a modified pBluescript vector
                     (FLC-1) as a BamHI/XhoI insert."
     gene            1..1279
                     /gene="At1g25560"
     misc_feature    66..1149
                     /gene="At1g25560"
                     /note="This may be a potential full length cDNA
                     corresponding to gene At1g25560. The cDNA contains a two
                     base pair deletion (GG) between positions 756 and 757
                     resulting in a truncated ORF."
     misc_difference 756..757
                     /gene="At1g25560"
                     /note="compared to genomic sequence"
                     /replace="ggga"
     misc_difference 1263
                     /gene="At1g25560"
                     /note="not present in genomic sequence"
ORIGIN
Query Match          30.1%;  Score 393.2;  DB 8;  Length 1279;
Best Local Similarity 64.5%;  Pred. No. 6.9e-76;
Matches    673;  Conservative    0;  Mismatches  328;  Indels  43;  Gaps    4;

Qy     159 CTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCCGATCAAGCGTTG 218
               |||  ||  |||||||||||||||     ||  |||||||||||||||| ||||||
Db     163 CTTCTCCGGCCGGCGACGTCGGATGCGTCCTACAGAATGGGAAGCCGGAAGCAGCAGCGTCG 222

Qy     219 TGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACA 278
               |||||||||||||||||||||| ||||     ||||||||
Db     223 TTTTGGATTCAGAGAACGGCGTCGAGACCGTCACGGTAAGCTTCCTTCGTCGAAAATATA 282

Qy     279 AAGGTGTGGTGCCACAACGAAGATGGGAGCTTCAGATTTACGAGAAGAAAACACCAGC 338
               ||||||||||||||||||||      ||  |||||||||||||||||||||||||||
Db     283 AAGGCGTTGTGCGCTCAGCTAACGAAGCGAAGATGGGAGCTTCAGATTTACGAGAAGCATCAGC 342

Qy     339 GGCGTGTGGCCTCGGGACATTCAACGAAGCGAAGAAGACGAAGCCGCTCGTCGTACGACGTCGCGG 398
               ||||||||||||||  |||||||||||||||||||||||||||||||   ||||
Db     343 GAGTTTGGCTCGTCGTTCAACGAGGAAGAAGAAGCTGCGTCTTCTTACGACATCGCCG 402

Qy     399 TTCACAGTTCCGTCGCCGTCGACGCCGTCACAAATTTCAAA---GACGTGAAGATGGACG 455
               ||| |||||||||| ||||||||||||||||||||||  ||||     |||||||||||||
Db     403 TGAGAGATTCCGCGCCGCGCCCGTCACTAACTTCAAATCTCAAGTGATGATTGGGAAACG 462

Qy     456 AAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAAATCGGAGATCGTTGATATGTTGAGGA 515
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Qy     628 GGGGTTTAGATCGGCGGAGGCACTCGTTGAGAAAGCCGGTAACCGGACGTCGGGAA 687
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Db   33722 GGGGTTTAAAACGGCGAGTTACTGTTTGAGAGAAACCGGTAACCGCCAAGTGACGTCGGGAA 33781

Qy     688 GCTAAACCGTTTGGTTATACCGAAACATCACGCGAGAGAAACATTTCCGTTACCGTCA-- 745
               ||||||||||||||||| |||||||| |||||||   | ||||||||||||||
Db   33782 ACTAAACCGTTTAGTTATATACCAAAACACCACCAAGCGGAGAAACATTTCCGTTACCGTTAGG 33841

Qy     746 ---AGTAACGTTTCCGTGAAAGGAGGTGTGTTGAACTTGAGGACGTAACGGGAAAGT 801
                  |||||||||||||  ||||  ||||||||||  ||||||||||||||||||||
Db   33842 TAATAATAACGTCTCCGTTAAAGGTATGCTGTTTGAATTTCGAAGACGTTAACGGGAAAGT 33901

Qy     802 GTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTG 861
               |||||||||||||||| |||||||||||||||  ||||||||||||| |||||||||
Db   33902 GTGGAGGTTCCGTTACTCTTTATTGGAATAGTAGTAGTCAAAGTTATGTGTTGACCAAAGGTTG 33961

Qy     862 GAGCAGGTTCGTTAAGGAAGAATCTACGTGCTGGGTGACGTGGTTAGTTTCAGTAGATC 921
               ||||||||||| |||||||||||  ||||||||| |||||| || |||||  |||||
Db   33962 GAGTAGATTCGTTAAAGACAGAGAAGACTTTGTGCGTGATTTGAATTCAGTTTAAAAGATC 34021

Qy     922 TAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTGA 981
               ||||||||||| |||||||||||| |||||| ||||||||||||||||||  ||||||
Db   34022 CAACGATCAAGATCAAAAATTCTTTATCGGGTGGAAATCGAAATCCGGGTTGGATCTAGA 34081

Qy     982 TGCGGGTCGGGTTTGAGATTGTTCGGAGTTAACATTTC 1020
               ||||||||||||| || |||||| ||| ||||||||
Db   34082 GACGGGTCGGGTTTATGAGATTGTTTGGGTTGGGGTTGATATTTC 34120

RESULT 10
AY056169
LOCUS       AY056169               1279 bp    mRNA   linear   PLN 23-SEP-2002
DEFINITION  Arabidopsis thaliana At1g25560 mRNA sequence.
ACCESSION   AY056169
VERSION     AY056169.1  GI:15810260
KEYWORDS    FLI cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1279)
  AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
            Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C.,
            Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R.,
            Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J.,
            Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
            Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K.,
            Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE     Arabidopsis Full Length cDNA Clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1279)
  AUTHORS   Yamada,K., Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M.,
            Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y.,
            Yu,G., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R.,
            Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G.,
            Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C.,
            Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
            Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S.E.,
            Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
REFERENCE   3  (bases 1 to 1279)
  AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
            Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K.,
            Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R.,
            Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J.,
            Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
            Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K.,
            Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE     Direct Submission
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TITLE        Arabidopsis Full Length cDNA Clones
JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 1376)
AUTHORS      Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
             Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
             Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
             Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
             Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,C.,
             Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
             Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
             Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE        Direct Submission
JOURNAL      Submitted (21-MAR-2002) Plant Gene Expression Center, 800 Buchanan
             Street, Albany, CA 94710, USA
COMMENT      RIKEN Genomic Sciences Center (GSC) members carried out the
             collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
             Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
             Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
             Hayashizaki,Y. and Shinozaki,K.

             The Salk, Stanford, PGEC (SSP) Consortium members carried out the
             sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J.,
             Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,
             Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
             Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,
             Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,
             Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,
             Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

             Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
             this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
             contributed equally to this work as PIs.

             Annotation is based on the January 2002 version of the Arabidopsis
             genome submitted to GenBank.
FEATURES             Location/Qualifiers
     source          1..1376
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /chromosome="1"
                     /clone="RAFL09-74-F02 (R19336)"
                     /ecotype="Columbia"
                     /note="This clone is in a modified pBluescript vector
                     (PLC-1) as a BamHI/XhoI insert."
     gene            1..1376
                     /gene="At1g25560"
     5'UTR           1..60
                     /gene="At1g25560"
     CDS             61..1146
                     /gene="At1g25560"
                     /codon_start=1
                     /evidence=experimental
                     /product="putative DNA-binding protein RAV2"
                     /protein_id="AAM13889.1"
                     /db_xref="GI:20259539"
                     /translation="MEYSCVDDSTTSESLSISTTPKPTTTBKKLSSPPATSMRLYR
                     MGSGGSSVVLDSENGVETESRKLPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEE
                     EEAASSYDIAVRRPRGRDAVTNFKSQVDGNDAESAFLDAHSKAEIVDMLRKHTYADEF
                     EQSRRKFVNGDGKRSGLETATYGNDAVLRAREVLFEKTVTPSDVGKLNRLVIPKQHAE
                     KHFPLPAMTTAMGMNPSPTKGVLINLEDRTGKVWRFRYSYWNSSQSYVLTKGWSRFVK
                     EKNLRAGDVVCFPRSTGPDRQLYIHWKVRSSPVQTVVRLFGVNIFNVSNEKPNDVAVE
                     CVGKKRSREDDLFSLGCSKKQAIINIL"
     3'UTR           1147..1376
                     /gene="At1g25560"
ORIGIN
Query Match     29.9%;  Score 391.2;  DB 8;  Length 1376;
Best Local Similarity   64.3%;  Pred. No. 1.9e-75;
Matches  673;  Conservative   0;  Mismatches 328;  Indels  45;  Gaps   4;

Qy   159 CTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACACGGAGGAGGGATCAAGCGTTG 218
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Db   463 ACGCCGGAATCGGCTTTCTTGACCTCATTCTAAAGCTGAGATCGTGGATATGTTGAGGA 522

Qy   516 AACATACTTATAACGGAAGAGTTAGAGCAGAGAGTAAACGGCGTCCTAATGTAACGGAAACA 575
             ||||| |||||   |||   || |||| | |||||||||  ||||||
Db   523 AACACACTTACGGCGATGAGTTTGAGCAGAGTAGACGGAAGTTGTTAACCGGCGACGGAA 582

Qy   576 TGACTAGGACGTTGTTAACGTCCGGGTTGAGGTAATGATGGTGTTCTACGACGGGGTTTA 635
             |||||  | ||||| |||| |  | ||  | ||||| ||| | |||| |||
Db   583 AACGGCTCTGGGTTGGAGACGGCGGACGTACGGAAACGACGCGCTGTT----------TTGA 630

Qy   636 GATCGGCGGAGGCACTGTTTGAGAAAGGCGGTAACGCCAAGCGACGTGGGAAGCTAAACC 695
             ||||||||||| || |||||||   ||||||  ||| || |||||||| |||  ||||
Db   631 GAGCGGCGTGAGGTTTGTTTGTTCGAGAGACTGTTACGTCCGAGCGACGTCGGGAAGCTGAACC 690

Qy   696 GTTTGGTTATACCGGAAACATCACGCCAGAGAAACATTTTCCGTTACGTCAAGTAACGTTT 755
             ||||| || || | ||| |  | |||  ||||||||  ||  ||||||| || ||||| |
Db   691 GTTTAGTGATACCGGAAACAACACGCGGAAGCATTTTCCGTTACCGGCGATGACGACGG 750

Qy   756 CCGT------------GAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGG 796
             | ||                |||  | ||  |  | || |||  | || |||
Db   751 CGATGGATGAATCCGTCTCCGACGAAAGGCGTTTTGATTAACTTGGAAGATAGAACAGGG 810

Qy   797 AAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCGTCAGAGTTATGTTTGACTAA 856
             |||||||| ||||||| | || | | || | |||||  ||   || ||||| |||| |
Db   811 AAAGTGTGGCGGTTCCGTTACTGGAACAGCAGTCGTCAAAGTTACGTGTTGACCAAG 870

Qy   857 GGTTGGAGCAGTTCGTTAAGGAGGAAGAATCTACGTGCTCGGTGACGTCGTTAGTTCAGT 916
             || ||||||| | |||| |||| ||||||  || ||  ||||| | | | | |||||
Db   871 GGCTGGAGCCGCGGTTCGTTAAAGAGGAAGAATCTTCGAGCCGGTGATGTGTTTGTTTCGAG 930

Qy   917 AGATCAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCGCAGAT 976
             ||||| |||| | ||  | || ||| ||| |||  | |||||| ||| |  ||||
Db   931 AGATCAACCGGCACCAGAGATCGTATATCCACTGGAAAGTCCGGTCTAGTCCGGTT 990

Qy   977 TTAGATGCGGGTCGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAGA 1036
             | | || | || | | |||| ||| |||| |||| ||| || ||||| || ||| ||
Db   991 CAGACTGTGTGTTAGGCTATTCGGAGTCAACGATTTCAATGTGAGTAACGAGAAACCAAAC 1050

Qy  1037 AACGACGTCGTA------------GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTG 1087
             |||||||| ||             || | ||||| |||| || |||| ||
Db  1051 GACGTCGCAGTAGAGTGTGTTGGCAAGAAGAGATCTCGGGAAGATGATTTGTTTTCGTTA 1110

Qy  1088 GTGTGTAGCAAGAAGCAAACGCATCTTCACGCCTCGTAACAACTCTTCTTTTTTTTTTTT 1147
             || | | |  ||  || |||  | ||| || ||| || | || ||   |
Db  1111 GGGTGTTCCAAGAAGCAGCAGGCGATTATCAACATCTTGTGACAAAATTCTTTTTTTTTGGTTT 1170

Qy  1148 TCTTTTGTTGTTTTAATAATTTT 1171
             |||||  ||| ||  |
Db  1171 TTTTTCTTCAATTTGTTTCTCCTT 1194
```

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RESULT 11
AY091069
LOCUS       AY091069                1376 bp    mRNA    linear   PLN 18-SEP-2002
DEFINITION  Arabidopsis thaliana putative DNA-binding protein RAV2 (At1g25560)
            mRNA, complete cds.
ACCESSION   AY091069
VERSION     AY091069.1  GI:20259538
KEYWORDS    FLI_cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1376)
AUTHORS     Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
            Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
            Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
            Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
            Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
            Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
            Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
            Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
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LOCUS         AC079281              102540 bp    DNA     linear   PLN 19-JAN-2001
DEFINITION    Arabidopsis thaliana chromosome 1 BAC F2J7 genomic sequence,
              complete sequence.
ACCESSION     AC079281
VERSION       AC079281.4  GI:12321495
KEYWORDS      HTG.
SOURCE        Arabidopsis thaliana (thale cress)
  ORGANISM    Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE     1  (bases 1 to 102540)
  AUTHORS     Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
              Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
              Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
  TITLE       Arabidopsis thaliana chromosome 1 BAC F2J7 genomic sequence
  JOURNAL     Unpublished
REFERENCE     2  (bases 1 to 102540)
  AUTHORS     Town,C.D. and Kaul,S.
  TITLE       Direct Submission
  JOURNAL     Submitted (26-AUG-2000) The Institute for Genomic Research, 9712
              Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
REFERENCE     3  (bases 1 to 102540)
  AUTHORS     Town,C.D. and Kaul,S.
  TITLE       Direct Submission
  JOURNAL     Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
              Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT       On Jan 19, 2001 this sequence version replaced gi:12280814.
              Address all correspondence to:at@tigr.org

              BAC clone F2J7 is from Arabidopsis thaliana chromosome 1
              The orientation of the sequence is from SP6 to T7 end of the BAC
              clone.
              Genes were identified by a combination of several methods: Gene
              prediction programs including Genscan+ (Chris Burge,
              http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
              http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
              of GlimmerM, see Mihaela Pertea,
              http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
              GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
              mpertea@tigr.org), searches of the complete sequence against a
              peptide database and the plant EST database at TIGR
              (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
              indicate the level of evidence for their annotation. Genes with
              similarity to other proteins are named after the database hits.
              Genes without significant peptide similarity but with EST
              similarity are named as  unknown  proteins. Genes without protein
              or EST similarity, that are predicted by more than two gene
              prediction programs over most of their length are annotated as
              hypothetical  proteins. Genes encoding tRNAs are predicted by
              tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
              Simple repeats are identified by repeatmasker (Arian Smit,
              http://ftp.genome.washington.edu/RM/RepeatMasker.html).
FEATURES             Location/Qualifiers
     source          1..102540
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="I"
                     /map="?"
                     /clone="F2J7"
     repeat_region   complement(356..382)
                     /rpt_family="(CATTA)n"
     repeat_region   complement(421..495)
                     /rpt_family="AT_rich"
     repeat_region   complement(897..1021)
                     /rpt_family="AT_rich"
     gene            2262..3272
                     /gene="F2J7.1"
                     /note="similar to hypothetical protein GI:7269821 from
                     (Arabidopsis thaliana)"
     mRNA            join(<2262..2360,2452..2638,2728..>3272)
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Db   158  CTTCTCCGCGGCGACGTCGATGCGTCTCCTACAGAATGGGAAGCGGCGGAAGCAGCGTCG  217
                                                                           
Qy   219  TGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACA  278
          | ||||||||| |||||  ||| |||||| ||  ||||| |||||| |||||||| |||
Db   218  TTTTGGATTCAGAGAACGGCGTCGAGACCGAGTCACGTAAGCTTCCTTCGTCGAAATATA  277
                                                                           
Qy   279  AAGGTGTGTGGCCACAACACCGAAGAGATGGGGAGCTCAGATTTACGAGAAACACCAGC   338
          ||||  |||| |||| |  ||| ||||| || |||||| ||||| ||||||||| ||||
Db   278  AAGGCCGTTGTGCCTCAGCCTAACGGAAGATGGGGAGCTCAGATTTACGAGAAGCATCAGC  337
                                                                           
Qy   339  GCGTGTCGGCTCGGGACATTCAACGAAGAGAGACGAAGCCGCTCCGTGCCTACGACGTCGCGG  398
          | |||||||  ||||| |||||||  ||||| |||||||||| || |||||| ||| | ||
Db   338  GAGTTTGGCTCCGTACTTTCAACGAGGAAGAAGCGTCGTCTTCTACGACATCGCCG  397
                                                                           
Qy   399  TTCACAGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAA---GACGTGAAGATGGACG  455
          |||||  ||| ||| |  ||| ||| ||||| |||| ||||   |||| |||||| |||
Db   398  TGAGGAGATTCCCGCGCCGCGACGCCCGTCACTAACTTCAAATCAAAATCACAGTTGATGGAAACG  457
                                                                           
Qy   456  AAGACAGAGGTCGATTTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGA  515
          |||||| |||| ||| |  || ||||| |||| ||| |||||| ||| ||||| | ||||
Db   458  ACGCCGAATCGGCTTTCTTCTTGACGCTCATTCTTAAAGCTGAGATCGTCGATATGTTGAGGA  517
                                                                           
Qy   516  AACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATCGTAACGGAGAAACA  575
          ||||  ||||| ||| |||||||| || | |  |||||||  | ||||| |||||| ||||
Db   518  AACACCATTACCGCCGATGAGTTTGAGCAGAGTAGACGGGAAGTTGTTAACGGGACGGGTTTA  577
                                                                           
Qy   576  TGACTAGGACGTTGTTAACGTCGGGGTGAGTAATGATGGTGTTTCTACGACGGGGTTTA  635
                                                            -------TTGA  625
          |||||| ||||| ||||| ||||||||  ||||| ||| ||  ||||||  ||||
Db   578  AACGGCTCTGGGTTTGGAGACGGCGGTAACGACGCTCGTT-------TTGA  625
                                                                           
Qy   636  GATCGCGGCGGAGGCACTGTTGAGAAAGCGGGTAACGCGCCAAGCGACGCGTTGGGAAGCTAAACC  695
          || ||||||| ||| |||||||||| ||| | |||||| |||||||| ||| |||||| ||||
Db   626  GAGCGCGTGAGGTTTTGTTCGAGAAGACTGTTACGCGCCAGCGACGTCGCGGGAAGCTGAACC  685
                                                                           
Qy   696  GTTTGGTTATACCGGAAACATCACGCAGCAGAGAAACATTTTCCGTTACCGTCAGTAACGTTT  755
          |||| | |||  ||||||| || |  || ||| |||| ||||||  ||| | ||||  ||
Db   686  GTTTAGTGATACCGGAAACAACAACGCGGAGAAGCAGCATTTTCCGTTACCGGCGGATGACGACGG  745
                                                                           
Qy   756  CCGT-----------GAAAGGAGTGTGTTGAACTTTGAGGACGTTAACG  794
          ||||           |||| || | |||  ||  | |||| ||||| |
Db   746  CGATGGGGATGAATCCGTCTCCGACGGAAGGCGTTTGATTAACTTGGAAGATAGAACAG  805
                                                                           
Qy   795  GGAAAGTGTGGAGGTTCCGTACTACTGGAACACAGTAGTCAGAGTTATGTTTGACTA  854
          ||||||||| | || || |||| ||| ||||| |  | ||| ||||| || |||
Db   806  GGAAAGTGTGGCGGCGGTTCCGTTCCGTTACAGTTACTGGAACAGCAGTCAAAGTTACGTGTTGACCA  865
                                                                           
Qy   855  AAGGTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTCGGTGACGTGGTTAGTTCA  914
          ||||| |||||  || ||| |||| |||||| | |||| |||||| |||  || |||
Db   866  AGGGCTGAGCCCGGTTCGTTAAAGAGAAGAATCTTCGAGCCCGGTGATGTGGTTGTTTTCG  925
                                                                           
Qy   915  GTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAG  974
          || | || |||| ||||||| ||||| | |||| ||| || |||||| ||||| |||
Db   926  AGAGATCAACCGGACCAGACCGGCAATTGTATATCCACTGGAAAGTCCGGTCTAGTCCGG  985
                                                                           
Qy   975  ATTTAGATGCGGGTCGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAA  1034
          || || ||| ||| |||| |||| ||| | ||||||| |||||| |||| |||  ||||
Db   986  TTCAGACTGTGGTTAGGCTATTCGGAGTCAACATTTTCAATGTGAGTAACGAGAAAACCAA  1045
                                                                           
Qy   1035 GAAACGACCTCGTA-------GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGT  1085
          || |||||| |                |||| ||||| | |||| | || ||||| ||
Db   1046 ACGACGTCGCAGTAGAGTGTGTTGGCAAGAGGATCTCGGAGAGATCGGGAAGATGATTGTTGTTTTCGT  1105
                                                                           
Qy   1086 TGGTGTGTAGCAAGAAAGCAACCGCATCTTTCACGCCTCGTAACAACTCTTCTTCTTTT  1145
          ||| ||  |||||| ||  || |  || |||| ||| ||||| ||| || |||||||||
Db   1106 TAGGGTGTTCCAAGAAGCAGCGGATTATCAACATCTTGTGACAAATTCTTTTTTTTGGT  1165
                                                                           
Qy   1146 TTTCTTTTGTTGTTTTTAATAATTTT  1171
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Db   1166 TTTTTTTCCTTCAATTTGTTCTCCTT  1191
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RESULT 12
AC079281

CDS

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                 KEKPKRADSQPLIKAITPTSTTTTSSTAETVGGGKEFBEQKQSHSNRKQRRCWSPELH
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                 30763. .30847,31189. .31275,31359. .>31862)
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                 VASNLGVSGVPMQMGQMNQGSHSGAMMQGGISMQNMSGLGQGNVSSGTGMMPTPGVGQ
                 QAQSGIQOLGGSNSSAPNMQLSQPSSGAMQTSQSKYVKWEGNLSGQRQGQPVLITRL
                 EGYRSASASDSLAANWPPTMQIVRLISQDHMNNKQYVGKADFIjVFRAMSQHGFLGQLQ
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                 /rpt_family="(CAG)n"
     gene        33863. .36641
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                 /note="similar to lysine and histidine specific
                 transporter GI:2576361 from (Arabidopsis thaliana)"
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                 GVHFILSOLPNFNSVAGVSLAAVMSLCYSTIAWGGSIAHGRVPSVDYKATNPGDF
                 TFRVFNALGQISFAFAGHAVALEIQATMPSTPERPSKVPMWQVIGAYVNAVCYFPV
                 ALICYWAFGQDVDDNVLMNLQRPAWLIAAANLMVVHVIGSYQVFAMPVFDLLERMMV
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Query Match   29.9%; Score 391.2; DB 8; Length 102540;
Best Local Similarity 64.3%; Pred. No. 2.6e-75;
Matches 673; Mismatches 328; Conservative 0; Indels 45; Gaps 4;

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Qy    159  CTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCGGATCAAGCGTTG  218
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Db  18375  CTTCTCCGCCGGCGACGTCGATGCCGTCTCTACAGAATGGAAGCGGCGGAAGCAGCGTCG  18434
Qy    219  TGTTAGATTCAGAGAACGGCGTAGAAGCTTAGGAAGCTTCCGTCGTCAAAATACA  278
                | || |||||||||||||||||||| | ||||||| ||||||| |||||| |||||
Db  18435  TTTTGGATTCAGAGAACGGCGTCGAGACCGAGTCACGTAAGCTTCCTTCGTCGAATATA  18494
Qy    279  AAGGTGTGGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAGAAACACCAGC  338
                ||||||| ||||| |||||| ||||| ||| ||||||| |||||| ||||||||  ||||
Db  18495  AAGGCGTTGTGCCTCAGCCTAACCGAAGATGGGAGCTCAGATTTACGAGAAGCATCAGC  18554
Qy    339  GCGTGGCTCGGGACATTCAACGAGAAGACGAAGCGGCCGCTCGTGCCTACGACGTCGCGG  398
                || | |||||| | || |||||||||||  |||| |||||  ||||  ||||||| ||||
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CDS

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                 VSHFFHKAIKAYSTGTRKRKRKIHDDDFGDVRWHKTGRTKPVVLDGVVQRGCKKIMVLYG
                 GKAVKTNWVMHQYHLGIEEDEKEGDYVVSKIFYQQPQQLVVKRGDKAEQEVSEDIFAA
                 VTPTADPVTPKLATPEPRNAVRICSDSHIASDYVTPSDYVSAHEVSLAEVRIFVVAFY
                 "
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                 /rpt_family="(GGA)n"
     gene        5962. .9353
                 /gene="F2J7.2"
     mRNA        join(5962. .6131,6272. .7030,7168. .7318,7695. .7766,
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                 /gene="F2J7.2"
     CDS         join(6673. .7030,7168. .7318,7695. .7766,7907. .7975,
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                 /protein_id="AAG50805.1"
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                 /translation="MKLYQTAVTVSGGGSLVELEVDAKLDYILLWFHFSEIDSTVKKA
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                 QGSALVIFQIDLGSQLKGFISEQISLLTNLNSINLSSNTLSGQLPLGLGHKSLVSLD
                 LSNNQLTGPIPBSLTLSSLKLVLLNGNELQGKVPEEVYSVGVHGGIIDASSKEKQIPB
                 AKVVDATGNGEFTRERNAHSSTEFAIAEKEK"
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                 (Arabidopsis thaliana)"
     mRNA        <18278. .>19363
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                 MGSGGGSSVVLDSENGVETESRKLPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEE
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                 EQSRRKFVNGDGKRSGLETATYGNDAVLRAREVLFEKTVTPSDVGKLNRLVIPKQHAE
                 KHFPLPAWTTAMGMNPSPTKGVLINLEDRTGKVWRFRYSYWNSSQSYVLTKGWSRFVK
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Db  18555 GAGTTTGGCTCGTACTTCAACGAGGAGAAGAAGCTGCGTCTTCTTACGACATCGCCG 18614
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Qy    399 TTCACAGGTTCCGTCCGTGAGCGCCGTCACAAATTCAAA---GACGTGAAGATGGACG 455
          ||| ||||    |  |      |||||||    ||||||
Db  18615 TGAGGAGATTCCGCGGCCGCGACGCCCGTCACTCACTTCAAATCCAAGTTGATGGAAACG 18674
Qy    456 AAGACAGAGTCGATTTCTTGAATTCTCATTCGAAATCTGAGACTCGTTGTGATATGTTGAGGA 515
          |||  ||||   |       |||  ||||       |  |||   |||||  |||||||||||
Db  18675 ACGCCGAATCGGCTTCTTCTTGACGCTCATTCTAAAGCTGAGATCGTCGATATGTTGAGGA 18734
Qy    516 AACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCCGTAATCGTAACGCGAAACA 575
          |||     ||||   |||||   |||||||   || ||||||| |  || |||| || |||
Db  18735 AACAACTTACGCGCCGATGAGTTTGAGCGACGGAAAGTTGTTAACGGCGACGGAA 18794
Qy    576 TGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTTA 635
          |||| ||| |||   ||||||||| |||      |||||| |||||  || ||||| |||
Db  18795 AACGGCTCTGGGTTGGAGACGCCGACGTACGGAAACGACGCTGTT---------TTGA 18842
Qy    636 GATCGCGGAGGACCACTGTTGAGAAAGGCGGTAACGCCCAAGCGACGTGGGAAGCTAAACC 695
          || ||||| | ||   ||||||  ||   |||||  |||| |||| |||  || |||| ||
Db  18843 GAGCGCGTGAGGTTTGTTCGAGAAGACTGTTACGCCGAGCGAGCGTCGGAAGCTGAACC 18902
Qy    696 GTTTGGTTATACCGGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTT 755
          ||||  ||| |||| |||||| |  ||||||||||||||||||||  || ||||| ||||
Db  18903 GTTTAGTGTATACCGGAAACAACACGGCGGAGAAGCATTTTCCGTTACCGGCGATGACGACGG 18962
Qy    756 CCGT------------GAAAGGAGTGTGTTGAAACTTTGAGGACGTTAACG 794
          ||||             |||  | ||||||||||||   |||||||| |||
Db  18963 CGATGGGGGATGAATCCGTCTCCCACGGAAAGGCGTTTTGATTAACTTGGAAGATAGAACAG 19022
Qy    795 GGAAAGTGGAGGTCCGGTTCCGTTACCTGTATTGGAACAGTAGCAGAGTTGTTTGGAACTA 854
          |||||| ||| ||| |    |||  ||| |||  |||||  ||| |||| |||| ||  ||
Db  19023 GGAAAGTGGTGGCGCCGGTTCGGTTACTACTGGAACAGCAGCAGTCAAAGTTACGTGTTGACCA 19082
Qy    855 AAGGTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTCGGTGACGTGGTTAGTTTCA 914
          |||   |||||||||| |||  |||||||||  |  |||| |||||| |||  ||| |||
Db  19083 AGGGCTGAGCGCCGGTTCGTTCGTTAAAGAGAAGAATCTTCGAGCCGCGTGATGTGGTTGTTTCG 19142
Qy    915 GTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAG 974
          || || || |  | |   |||||| ||||| |||  |||||||||||| || |||  |
Db  19143 AGAGATCAACCGGACCAGACCGGCAATTGTATATCCACTGGAAAGTCCGGTCTAGTCCGG 19202
Qy    975 ATTTAGATGCGGGTCGGGGTTTGAGATGTGTTCGGAGTTAACATTTCACCGGAGAGTTCAA 1034
          ||| |||| ||||| ||||| |||||| ||| |||||||||||||||||  |||||| |||
Db  19203 TTCAGACTGTGGTTAGGCTATTCGGAGTCAACATTTTCAATGTGAGTAACGAGAAACCAA 19262
Qy   1035 GGAAACGACGTCGTA---------GGAAACAAAGAGTGAACGATACTCGAGATGTTATCGT 1085
          |||||| ||| |||          ||||   || |||  |||| ||||  |||||| ||||
Db  19263 ACGACGTCGCAGTAGAGTGTTGGCAAGAAGATCTCGGGAAGATGATTTGTTTTTCGT 19322
Qy   1086 TGGTGTGTAGCAAGAAGCAACGCATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTT 1145
          ||  || ||||||||| |||  | || |||||  | |||| ||||| || |||||||||
Db  19323 TAGGGTGTTCCAAGAAGCAGGCGGATTATCAACATCTTGTGACAAATTCTTTTTTTTGGT 19382
Qy   1146 TTTCTTTTGTTGTTTTAATAATTTT 1171
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Db  19383 TTTTTTTTCTTCAATTGTTTCTCCTT 19408
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RESULT 13
AY122941

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LOCUS       AY122941                1117 bp    mRNA            linear   PLN 18-SEP-2002
DEFINITION  Arabidopsis thaliana putative DNA-binding protein RAV2 (At1g25560)
            mRNA, complete cds.
ACCESSION   AY122941
VERSION     AY122941.1  GI:21689704
KEYWORDS    FLI cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1117)
```

AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
          Lee,J.M., Quach,H.L., Tang,C., Toriumi,M., Wu,H.C., Yu,G.,
          Bowser,L., Carninci,P., Chen,H., Cheuk,R., Karlin-Neumann,G., Kawai,J.,
          ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
          Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
          Palm,C.J., Sakurai,T., Satou,M., Shinn,P., Southwick,A.,
          Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE   Arabidopsis Open Reading Frame (ORF) Clones
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 1117)

AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
          Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yu,G.,
          Bowser,L., Carninci,P., Chen,H., Cheuk,R., Karlin-Neumann,G., Kawai,J.,
          ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
          Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
          Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
          Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE   Direct Submission
JOURNAL   Submitted (17-JUN-2002) Plant Gene Expression Cencer, 800 Buchanan
          Street, Albany, CA 94710, USA

COMMENT   The RIKEN Genomic Sciences Center (GSC) members carried out the
          collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
          Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., ishida,J.,
          Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
          Hayashizaki,Y. and Shinozaki,K.

          The Salk, Stanford, PGEC (SSP) Consortium members constructed and
          sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K.,
          Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M.,
          Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yu,G., Bowser,L.,
          Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B.,
          Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
          Davis,R.W., Ecker,J.R. and Theologis,A.

          Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
          to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
          /PGEC) contributed equally to this work as PIs.

          Annotation is based on the January 2002 version of the Arabidopsis
          genome submitted to GenBank.
FEATURES   Location/Qualifiers
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     CDS   1..1086
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                     /gene="At1g25560"
ORIGIN

Query Match   29.8%;   Score 389.8;   DB 8;   Length 1117;
Best Local Similarity 64.8%;   Pred. No. 3.8e-75;
Matches 665;   Conservative 0;   Mismatches 317;   Indels 45;   Gaps 4;

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RESULT 14
         AC011914/c
LOCUS       AC011914               96808 bp    DNA     linear   PLN 19-JAN-2001
DEFINITION  Arabidopsis thaliana chromosome 1 BAC F14K14 genomic sequence,
            complete sequence.
ACCESSION   AC011914
VERSION     AC011914.9  GI:12324129
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 96808)
  AUTHORS   Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
            Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
            Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
  TITLE     Arabidopsis thaliana chromosome 1 BAC F14K14 genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 96808)
  AUTHORS   Lin,X. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-OCT-1999) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
REFERENCE   3  (bases 1 to 96808)
  AUTHORS   Town,C.D. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
            On Jan 19, 2001 this sequence version replaced gi:12280763.
            Address all correspondence to:at@tigr.org
COMMENT     BAC clone F14K14 is from Arabidopsis thaliana chromosome 1
            The orientation of the sequence is from SP6 to T7 end of the BAC
            clone.
            Genes were identified by a combination of several methods: Gene
            prediction programs including Genscan+ (Chris Burge,
            http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
            http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
            of GlimmerM, see Mihaela Pertea,
            http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
            GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
            mpertea@tigr.org), searches of the complete sequence against a
            peptide database and the plant EST database at TIGR
            (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
            indicate the level of evidence for their annotation. Genes with
            similarity to other proteins are named after the database hits.
            Genes without significant peptide similarity but with EST
            similarity are named as unknown proteins. Genes without protein
            or EST similarity, that are predicted by more than two gene
            prediction programs over most of their length are annotated as
            hypothetical proteins. Genes encoding tRNAs are predicted by
            tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
            Simple repeats are identified by repeatmasker (Arian Smit,
            http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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                     /gene="F14K14.1"
                     /note="similar to bZIP DNA-binding protein GB:AAD55394
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Qy  159 CTCCGGCGAAAAAGTCGTCGTAGTAACTTATACAGGATGGGAAGCCGATCAAGCGTTG  218
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Db   98 CTTCTCCCCGCGGCGACGTCGATGCGTCTCTACAGAATGGGAAGCGGCCGAAGCAGCGTCG  157

Qy  219 TGTTAGATTCAGAGAACGGCGTAGAAGTGAATCTAGGAAGCTTCCGTCGTCAAAATACA  278
            | || ||||||||||||||||| ||||  ||  ||  ||||| ||  |||| || |||| |
Db  158 TTTTGGATTCAGAGAACGGCGTCGAGACCGAGTCACGTAAGCTTCCTTCGTCGAAATATA  217

Qy  279 AAGGTGTGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAGAAAACACCAGC  338
            ||||  |||||||| || | || ||||||||  |||||||||||||||| || |||||
Db  218 AAGGCGGTTGTGCCTCAGCCTCAACGGAAGATGGGGAGCTCAGATTTACGAGAAGCATCAGC  277

Qy  339 GCGTGGCTCGGGACAATTCAACGAAGAAGACCAAGCCGCTGTGCCTACGACGTCGCCGG  398
            | || ||||||  || |||||||| |||||| || |  |||   || |||| | ||| ||
Db  278 GAGTTTGGCTCGGTACTTTCAACGAACGAAGAAGCGTCGTCGTCTTCTTACGACATCGCCG  337

Qy  399 TTCACAGGTTCCGTCGCCGTGACCGCCGTCACAAATTCAAA---GACGTGAAGATGGACG  455
            |  | ||||||||  | || ||| || |||||   ||||||       |||  ||||| ||
Db  338 TGAGGAGATTCCGCGCGCCGCGACGCCGTCACTAACTTCAAATCTCAAATCTCAAGTTGATGGAAACG  397

Qy  456 AAGACGAGGTCGATTTCTTGAAATCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGA  515
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Db  398 ACGCCGAATCGGCTTTTCTTGACGCTCTCAAAGCTCTCAAAGCTGAGATCGTGGATATGTTGAGGA  457

Qy  516 AACATACTTATAACGAAGAGTTAGAGCAGCAGAGTAAACGGCGTCGTAAATGGTAACCGAAACA  575
            || ||| ||   |||| |||| || ||||||||| |||||||  | ||||||| | ||| ||||
Db  458 AACACACTTACGCCGATGAGTTTGAGCAGCAGACGAGGAAGTTTGTTAACGGGCGACGGAA  517

Qy  576 TGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGGTTTA  635
            |||  | |||  | ||  |||| |||||| || ||| ||||  | || ||| ||
Db  518 AACGGCTCGGGTTGGAGACGGCGCGACGTACCGGAAACGACGCCTGTT--------TTGA  565

Qy  636 GATCGGCGGAGGCACTGTTGAGAAGCCGTAACGCCAAGCGACGTTGGGAAGCTAAACC  695
            ||   |  | |||||| ||||||||||||  | ||  |||||||| | |||||| ||||
Db  566 GAGCGGCGTGAGGTTTTGTTCGAGAAGACTGTTACGCCGGAGCGACGTCGGGAAGCTGAACC  625

Qy  696 GTTTGGTTATACCGGAAACATCACGCGACAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTT  755
            ||| | ||||  ||||||  || || |||||||| ||| ||  |||| ||||| | ||||| ||
Db  626 GTTTAGTGATACCGGAAACAACACGCGGAGAAGCATTTTCCGTTACCGGCGGCATGACGACGG  685

Qy  756 CCGT-----------------GAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACG  794
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Db  686 CGAATGGGGATGAATCCGTCTCCGACGAAAGGCGTTTGATTAACTTGGAGAAGATAGAAACAG  745

Qy  795 GGAAAGTGTGGAGGTTCCGTTCCGTTACTTCGTATTGGAACAGTAGACAGTTATGTTTGACTA  854
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Db  746 GGAAAGTGTGGCGGTTCCGTTACTTCGGTTACAGTTACGACAGCAGTTACGTGTTTGACCA  805

Qy  855 AAGGTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTGGTGGACGTGGTTAGTTTCA  914
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Db  806 AGGGCTGGAGCCGGTTCGTTAAAGGAGAAGAATCTTCGAGCCCGGTGATGTGGTTGTTTCG  865

Qy  915 GTAGATCTAACGGTCAGGATCAACATTGTATCAATGTTATATCACCTGGAAAGTCCGGTCAG  974
            |   | || |  || | ||| |||| || | | ||||| |||  | || |||||||| ||||
Db  866 AGAGATCAACCGGACCGGACCGGCAATTGTATATCACTGGAAAGTCCGGTCTAGTCCGG  925

Qy  975 ATTTAGATCGCGGTCGGGTTTTGAGATTGTTCGGAGATTGTTAACATTCACCGGAGAGTTCAA  1034
            | | |||| |  | ||| || ||| || ||| |||| |  | || || | ||| ||| ||||
Db  926 TTCAGACTGTGGTTAGGCTATTCGGAGCTATTCGAGAGTCAACATTTCAATGTGAGTAACGAGAAACCAA  985

Qy 1035 GAAACGACGTCGTA-------GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGT  1085
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Db  986 ACGACGTCCGCAGTGAGTGTGTTGGCAAGAAGATCTCGGAGAGATGATTTGTTTTCGT  1045

Qy 1086 TGGTCGTGTAGCAAGAAGCAACGCATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTT  1145
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Db 1046 TAGGGTGTTCCAAGAGCAGGCAGGCGATTATCAACATCTTGTGACAAATTCTTTTTTTTGGT  1105

Qy 1146 TTTCTTT  1152
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                  /protein_id="AAG52032.1"
                  /db_xref="GI:12324131"
                  /translation="MAGSVVNLPSQNPNPQOSLFQIFVDRVPLSNLPATSDDSSRTAED
                  NERKRRRKVSNRESAARSRMRKQRHMEELWSMLVQLINKNKSLVDELSQARECYEKVI
                  BENMKLREENSKRKMIGEIGLNRFLSVEADQIWTF"

gene              complement(7929..8372)
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mRNA              complement(<7929..>8372)
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                  /note="predicted by genefinder"

CDS               complement(7929..8372)
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repeat_region     8172..8222
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gene              complement(10880..10953)
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tRNA              complement(10880..10953)
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                  /note="identical to peroxidase ATP23a GB:CAA70035,
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CDS               join(12312,12638..12829,12950..13115,13256..13683)
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                  VIKKEMBCIVKEDPRNAAIIIRLHFHDCFVQGCDGSVLLDETETLQGEKRASPNINSL
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                  LATTNLPTPEEGLISIIAKFYSQGLSVEBMVALIGAHTIGKAQCRNFRSRIYGDFQVT
                  SALNPVSETYLASLREICPASSGEGDSNVTAIDNVTPNLFDNSIYHTLLRGEGLLNSD
                  QEMYTSLFGIQTRRIVSKYAEDPVAFFEQFSKSMVKMGNILNSESLADGEVRRNCRFV
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repeat_region     complement(15498..15517)
                  /rpt_family="(A)n"

gene              complement(15827..17141)
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                  DNA-binding protein: Nucleic Acids Res 1999 Jan
                  15;27(2):470-8)"

mRNA              complement(<15827..>17141)
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CDS               complement(15989..17047)
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                  /codon_start=1
                  /product="RAV2; 17047-15989"
                  /protein_id="AAG52035.1"
                  /db_xref="GI:12324134"
                  /translation="MDSSCIDEISSSTSESFSATTAKKLSPPPAAALRLYRMGSGSS
                  VVLDPENGLETESRKLPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEQEEAARSY
                  DIAACRFRGRDAVVNFKNVLEDGDLAFLEAHSKABIVDMLRKHTYADELEQNNKRQLF
                  LSVDANGKRNGSSTTQNDKVLKTREVLFEKAVTPSDVGKLNRLVIPKQHAEKHFPLPS
                  PSPAVIKGVLINFEDVNGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNLRAGDVVTFE
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                  kinase domain"

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                  /gene="F14K14.6"

CDS               join(22015..22407,22500..22586,22667..22786,22867..22965,
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                  EGEYVLKKATEYGAVEIWMNERVRRACGNSCADFVGFLDKSSKKGPEYWLIWKYEGE
                  STLAGLMQSKEFPYNVETIILGKVQDLPKGLERENKIIQTIMRQLLFALDGLHSTGII
                  HRDVKPQNIIFSEGSRSFKIIDLGAAADLRVGINYIPKEFLLDPRYAAPEQYIMSTQT
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                  DYDLTAWRKLVEPRASADLRRGFELVDLDGGIGWELLTSMVRYKARQRISAKAALAHP
                  YFDRQGLLALSVMQNLRMQYFRATQQDYSRAANWVIQLMAKNGTEKDGGFTETQLQEL
                  REKEPRKKANAQRNALASALRLQRKLVKTVTETIDEISDGRKTVWNRWIPREE"

gene              complement(28688..29936)
                  /gene="F14K14.7"
                  /note="C-term similar to C-term of apoptosis inhibitor
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CDS               complement(join(28688..28766,28868..28947,29038..29118,
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                  RYFTATSSAREFLGFFQHGARLLGWWSIDEGSREEQARLYSGEATGYNTFSPEVVKKM
                  PKSDLVEBIWRLQAALSEQTDITSYSQOEYERLQNEKILCRVCPEDPINVLLPCRHH
                  VLCSTCCEKKCKCPICRVLIERRMPYYDV"

repeat_region     complement(32255..32289)
                  /rpt_family="AT_rich"

repeat_region     complement(33272..33299)
                  /rpt_family="AT_rich"

gene              complement(34606..36199)
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Best Local Similarity   62.7%;  Pred. No. 1e-72;
Matches   741;  Conservative   0;  Mismatches  396;  Indels  44;  Gaps   8;

Qy      43 ATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAA--AACACAGATTAAATGGAATCG 100
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Db   17098 ATTTTTGTTTCTTGGTGTTGGTGAGAATCTTCAAGAAACTGAAACAAAGAAAATGGATTCT 17039

Qy     101 AGTAGCGTTGATGAG---AGTACTACAAGTACAGGTTCCATCTGTGAAACCCCGC---- 153
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Db   17038 AGTTGCATAGACGAGATAGTTCCTCCACTTCAGAATCTTCTCCGCGACCACCGCCAAG 16979

Qy     154 --GATAACTCCGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCGGATCA 211
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Db   16978 AAGCTCTCTCCTCCTCCCGCGGCGGCGTTACGCCTCTACCGGATGGGAAGCGGGCGGAGC 16919
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Tue Sep 13 10:10:51 2005

us-10-632-436a-1.rge

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ACCESSION   AC011665
VERSION     AC011665.8  GI:12323207
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 100515)
  AUTHORS   Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
            Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
            Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
  TITLE     Arabidopsis thaliana chromosome 1 BAC T6L1 genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 100515)
  AUTHORS   Lin,X. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-OCT-1999) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
REFERENCE   3  (bases 1 to 100515)
  AUTHORS   Town,C.D. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT     On Jan 19, 2001 this sequence version replaced gi:12280894.
            Addres all correspondence to:at@tigr.org

            BAC clone T6L1 is from Arabidopsis thaliana chromosome 1
            The orientation of the sequence is from SP6 to T7 end of the BAC
            clone.
            Genes were identified by a combination of several methods: Gene
            prediction programs including Genscan+ (Chris Burge,
            http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
            http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
            of GlimmerM, see Mihaela Pertea,
            http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
            GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
            mpertea@tigr.org), searches of the complete sequence against a
            peptide database and the plant EST database at TIGR
            (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
            indicate the level of evidence for their annotation. Genes with
            similarity to other proteins are named after the database hits.
            Genes without significant peptide similarity but with EST
            similarity are named as unknown proteins. Genes without protein
            or EST similarity, that are predicted by more than two gene
            prediction programs over most of their length are annotated as
            hypothetical proteins. Genes encoding tRNAs are predicted by
            tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
            Simple repeats are identified by repeatmaker (Arian Smit,
            http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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                     /cultivar="Columbia"
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                     /chromosome="1"
                     /clone="T6L1"
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                     /rpt_family="(TA)n"
     repeat_region   complement(1046..1089)
                     /rpt_family="AT_rich"
     repeat_region   1501..1592
     repeat_region   complement(1833..1879)
                     /rpt_family="(CAT)n"
     gene            2929..4522
                     /gene="T6L1.1"
                     /note="Pfam HMM hit: helix-loop-helix DNA-binding domain"
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Db 16918 AGCGTCGTGTTGGATCCCGAGAACGCGCTAGAGACGGGCGAGTCACGAAAGCTACCATCTTCA 16859

Qy   272 AATACAAAGGTGTGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAGAAA 331
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Db 16858 AAATACAAAGGGTGTTCCTCAGCCTAACGGAAGATGGGAGCTCAGATCTACGAGAAG 16799

Qy   332 CACCAGGCGCGTGTGGCTCGGACATTCAACGAAGCAGAAGACGAAGCCGCGTCGTGCCTACGAC 391
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Db 16798 CACCAACGAGTATGGCTCGGGACTTTCAACGAACGAGCAAGAAGAAGCCTGCTCGTTCGTTCCTACGAC 16739

Qy   392 GTCGGCGGTTCACAGGTTCCGTCGCGCGGTCACGCCGTGCACAATTCAAAGACGTGAAGATG 451
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Db 16738 ATCGGCAGCTTGTGTAGATTCCGTGGCCGCCGGAGCGGCCGTCGTCAACTTCAAGAACGT---TCTG 16682

Qy   452 GACGAAGACGAGGTCGATTCTTGATTTCTCATTCGAAATCTGAGATCGTTGATATGTTG 511
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Db 16681 GAAGACGCGCGATTTAGCTTTCTTGAAGCTCACTCAAAGCCCGAGATCGTCGACATGTTG 16622

Qy   512 AGGAAACATACTTATAACGAAGAGTTAGAGCAGCAGAGTAAACGGCGTCGTAATGGTAACCGA 571
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Db 16621 AGAAAACACACTTTACGCCGACGAGCTTGAACAGAACAATAAACGGCAGTTGTTTCTCTCC 16562

Qy   572 AACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGG 631
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Qy   632 TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTA 691
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Qy   692 AACCGTTGGTTATACCGGAAACATCACGCGAGAAAACATTTCCGTTACCGTCAAGTAAC 751
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Qy   752 GTTTCCGTG---AAAGGAGTGTGTTGAACTTTGAACTTGAACGGGAAAGTGTGGAGG 808
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Db 16387 CCGGCAGTGACTAAAGGAGAGTTTGTGATCAACTTCGAAGACGTTAACGTAAGGTGTGGGAGG 16328

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
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Db 16327 TTCCGTTACTCATACTGGACACGTAGTCAGAGTTACGTCGTTGACCAAGGGATGGAGTCCA 16268

Qy   869 TTCGTTAAGGAGAGAATCTACGTGCTCGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
         ||||||||||||||||||||| |||| ||| |||||||||||||||||||||||||||
Db 16267 TTCGTCAAGGAGAAGAATCTTCGAGCCGTGGTGATGTTGTTACTTTCGAGAGATCGACCGGA 16208

Qy   929 CAGGATCAACAGTTGTACATTGGGGTGGAA-----------GTCGAGATCGCGGGTCAGAT 976
         |||||||||||||||| ||| |||| ||| ||||
Db 16207 CTAGAGCCGCAGTTATATATTGATTGGAAAGTTCGGTCGGTCCGAGAGAAAAACCCGGTT 16148

Qy   977 TTAGATGCCGGTCCGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGA 1036
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Db 16147 CAGGTGGTGGTGTTCCGGCTTTTCGGAGTTGATATCTTTAATGTGACCACCGTGAAGCCAAAC 16088

Qy 1037 AACGACGT-------CGTAGGAACAAAAGAGTGAACCATACTGAGATGTTATCGTTG 1087
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Db 16087 GACGTCGTCGCCGTTCGCGGTGAGAAAGACTCGAGATGTTGATGATATGTTTGCGTTA 16028

Qy 1088 GTGTGTAGCAAGAAGCAACCACCGATCTTCACGCCTCGTAACAACTCTTCTTTTTTTTTT 1147
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Db 16027 CGGTGTTCCAAGAACGCAGGCGCGATAATCAATGCTTTGTGACATATTTCCTTTTCCGATTTT 15968

Qy 1148 TCTTTTGTTGTTTAATAATTTTTAAAAACTCCATTTCGT 1188
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RESULT 15
AC011665
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DEFINITION Arabidopsis thaliana chromosome 1 BAC T6L1 genomic sequence,
            complete sequence.

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gene                21988..23302
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Query Match           29.0%;    Score 379.4;    DB 8;    Length 100515;
Best Local Similarity  62.7%;    Pred. No. 1e-72;
Matches   741;  Conservative   0;  Mismatches   396;  Indels   44;  Gaps    8;

Qy      43 ATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAA--AACACAGATTAAATGGAATCG 100
           |||||| ||||| ||||| |||||||| ||||||||  ||||||||| ||||||||||||
Db   22031 ATTTTGTTTCTTGGTTTGGTGAGAATCTTCAAGAAACTCAGAAAACAAAGAAAATGGATTCT 22090

Qy     101 AGTAGCGTTGATGAG----AGTACTACAAGTACAGGTTCCATCTGTGAAACCCCGGC---- 153
           ||||| |||||||||    |||||||| |||||||||||||||||||||||||||||
Db   22091 AGTTGCATAGACAGATAAGTTCCTCCACTTCAGAATCTTTCTCCGCCACCACCCCAAG 22150

Qy     154 --GATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACACAGGATCGGAAGCGGGATCA 211
             ||||||||||||||| |||||||||||||||| ||||||| |||||||||||||||
Db   22151 AAGCTCTCCTCCTCCGCGCGGCGTTACGCCTCTACCCGGATGGGAAGCGGGGGAGC 22210

Qy     212 AGCGTTGTTGTTAGATTCAGAGAACGAGCGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCA 271
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Db   22211 AGCGTCGTTGTTGGATCCCGAGAACGCGGCAGCGAGTCAGACGCGGACCGGAGTCACCATCTTCA 22270
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Tue Sep 13 10:10:51 2005

us-10-632-436a-1.rge

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Qy    272  AAATACAAAGGTGTGGTGCCACCAACCAAACGGAAGATGGGGAGCTCAGATTTACGAGAAA  331
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Db  22271  AAATACAAAGGTGTTGTTCCTCAGCCTAACGGAAGATGGGGAGCTCAGATCTACGAGAAG  22330

Qy    332  CACCAGCCGCGTGTGGCTCGGGACATTCAACGAAGACGAAGCGCGTCGTGCCTACGAC    391
           ||||| || | || || ||||| || |||||  |||||||||| |||  ||||||||||
Db  22331  CACCAACGAGTATGGCTCCGGGACTTTCAACGAGCAAGAAGAAGCTGCTCGTTCCTACGAC  22390

Qy    392  GTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAGATG  451
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Db  22391  ATCGCAGCTTGTAGATTCCGTGGCCGCGGACGCCGTCGTCAACTTCAAGAACGT---TCTG  22447

Qy    452  GACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTG  511
              ||| || |  |||| ||||| |||||  |||| ||||||||||| |||||| ||| |
Db  22448  GAAGACGGCGGATTTAGCTTTCTTGAAGCTCACTCAAAGGCCGGAGATCGTCGACATGTTG  22507

Qy    512  AGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAATGTAACCGGA  571
           |||||||| | ||| ||| ||  | ||| || |||| ||||||| |||||||| |||||
Db  22508  AGAAAACACACTTACGCCGACGAGCTTGAACAGAACAATAAACGGCAGTTGTTTCTCTCC  22567

Qy    572  AACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTCTACGACGGGG    631
           |||| | || |  |  ||||||||| ||| ||||  ||| || ||        |||||||
Db  22568  GTCGACGCTAACGGAAAACGTAACGTAGGATGAGTACTCAAAACG------ACAAAGTT  22621

Qy    632  TTTAGATCGGCGGAGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTA  691
           |||| ||| ||||||| ||  ||||||||||  ||||| || |||||||||| ||||||
Db  22622  TTAAAGACGCGTGAAGTTCTTTTCGAGAAGGCGTTGACACCTAGCGACGTTGGGAAGCTA  22681

Qy    692  AACCGTTTGTTATACGGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAAC  751
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Qy    752  GTTTCCGTG---AAAGGAGTCGTGTTGAACTTGAGGACGTTAACGGGAAAGTGTGGAGG  808
                  |||   |||| | |||| |  |||||| ||||| ||||||| ||||| |||||||
Db  22742  CCGGCAGTGACTAAAGGAGTTTTGATCAACTTCGAAGACGTTAACGGTAAAGTGTGGAGG  22801

Qy    809  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG  868
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Db  22802  TTCCGTTACTCATACTGGAACAGTAGTCAAAGTTACGTGTTGACCAAGGGATGGAGTCGA  22861

Qy    869  TTCGTTAAGGAGAAGAATCTCACGTGCTCGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT  928
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Db  22862  TTCGTCAAGGAGAAGAATCTTCGACCCGGTGATGTTGTTTACTTTCGAGAGATCGACCGGA  22921

Qy    929  CAGGATCAACAGTTGTACATTGGGTGGAA-------------GTCGAGATCCGGGTCAGAT  976
           | || ||| |||  | ||  ||| ||||            ||||| || |||||| ||
Db  22922  CTAGAGCGGCAGTTATATATTGATTGGAAAGTTCGGTCCGAGAGAAAACCCGGTT  22981

Qy    977  TTAGATGCGGGTCGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGA  1036
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Qy   1037  AACGACGT--------CGTAGGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTG  1087
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Qy   1088  GTGTGTAGCAAGAAGCAACGACCATCTTCAGCCCTCGTAACAACTCTTCTTCTTTTTTTTT  1147
           ||| || |||||| ||||||  |  ||||  || |  |  |||  || |||| |||||||
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Qy   1148  TCTTTTGTTGTTTAATAATTTTTAAAAACTCCATTTTCGT  1188
              || |||  | |||||  |||| ||  || |||||| |
Db  23162  ATGCTTTCGTTTTTTAATTTTTTTTTTTTTTGTCAAGTTGTGT  23202
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Search completed: September 11, 2005, 02:50:38
Job time : 6003.04 secs

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                    GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   September 10, 2005, 20:12:16 ; Search time 799.949 Seconds
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Title:          US-10-632-436A-1
Perfect score:  1308
Sequence:       1 gatacatatacacaacata........ttaaaagggtacttagat 1308

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:     8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	1308	100.0	1308	12	ADM13467	Adm13467 Arabidops
2	1308	100.0	3835	10	ABT16588	Abt16588 Ethylene
3	1255	95.9	1281	4	AAD05842	Aad05842 Arabidops
4	1255	95.9	1281	5	AAD06649	Aad06649 A. thalia
5	1255	95.9	1281	6	ABK65156	Abk65156 Arabidops
6	1255	95.9	1281	9	ADA15448	Ada15448 DNA encod
7	1255	95.9	1281	9	ACD98391	Acd98391 A. thalia
8	1255	95.9	1281	10	ADB31784	Adb31784 DNA encod
9	1255	95.9	1281	10	ADD55665	Add55665 Thalecres
10	1255	95.9	1281	10	ADD30762	Add30762 Plant yie
11	1255	95.9	1281	10	ADE37198	Ade37198 Plant yie
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13	1255	95.9	1281	12	ADI41706	Adi41706 Plant tra
14	1255	95.9	1281	12	ADO02166	Ado02166 Thalecres
15	1255	95.9	1281	12	ADP67768	Adp67768 Arabidops
16	1035	79.1	1035	6	ABZ14511	Abz14511 Arabidops
17	971.8	74.3	1003	6	ABN98461	Abn98461 Arabidops
c 18	527.4	40.3	573	3	AAC32867	Aac32867 Arabidops
19	517.8	39.6	1155	4	AAD05843	Aad05843 Arabidops
20	517.8	39.6	1155	5	AAD06665	Aad06665 A. thalia
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22	517.8	39.6	1155	10	ADD30387	Add30387 Plant yie
23	517.8	39.6	1155	10	ADE37138	Ade37138 Plant yie
24	517.8	39.6	1155	10	ADE31464	Ade31464 Plant yie
25	517.8	39.6	1155	12	ADI41906	Adi41906 Plant tra
26	517.8	39.6	1155	12	ADO03478	Ado03478 Thalecres
27	517.8	39.6	1155	12	ADP67774	Adp67774 Arabidops
28	517.8	39.6	1235	3	AAC50721	Aac50721 Arabidops
29	517.8	39.6	1244	3	AAC40426	Aac40426 Arabidops
30	517.8	39.6	3802	10	ABT16587	Abt16587 Ethylene
c 31	493.8	37.8	969	12	ADP67808	Adp67808 Cauliflow
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33	391.2	29.9	3886	10	ABT16585	Abt16585 Ethylene
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36	389.8	29.8	1239	6	ABK65329	Abk65329 Arabidops
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38	389.8	29.8	1239	10	ADB31802	Adb31802 DNA encod
39	389.8	29.8	1239	10	ADD30545	Add30545 Plant yie
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41	389.8	29.8	1239	12	ADO03414	Ado03414 Thalecres
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43	389.8	29.8	1239	13	ADI43608	Adi43608 Plant tra
44	379.4	29.0	3859	10	ABT16586	Abt16586 Ethylene
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ALIGNMENTS

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RESULT 1
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ID   ADM13467 standard; cDNA; 1308 BP.
XX
AC   ADM13467;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Arabidopsis AP2 domain transcription factor RAV1 cDNA.
XX
KW   plant growth regulant; chimeric plant-expressible gene; plant;
KW   mRNA transcription; freezing tolerance; drought tolerance;
KW   transcription regulating protein; binding protein; AP2 domain;
KW   cold regulatory gene; dehydration regulatory gene; RAV1; gene; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US2004078852-A1.
XX
PD   22-APR-2004.
XX
PF   01-AUG-2003; 2003US-00632436.
XX
PR   02-AUG-2002; 2002US-0400777P.
XX
PA   (THOM/)  THOMASHOW M F.
PA   (FOWL/)  FOWLER S G.
PA   (VOGE/)  VOGEL J.
PA   (ZARK/)  ZARKA D.
XX
PI   Thomashow MF,  Fowler SG,  Vogel J,  Zarka D;
XX
DR   WPI; 2004-340088/31.
XX
PT   Chimeric plant expressible gene encoding a cold-regulated transcription
PT   factor ( ZAT12 or RAV1), is useful in inducing freezing or drought
PT   tolerance in a plant.
XX
PS   Claim 3; SEQ ID NO 1; 52pp; English.
XX
CC   The invention describes a chimeric plant-expressible gene comprising in
CC   the 5' to 3' direction: (a) a promoter capable of effecting mRNA
CC   transcription in the selected plant cell to be transformed, operably
```

CC   linked to (b) a structural DNA sequence encoding the 1308bp sequence
CC   (SEQ. ID. No. 1) or 816bp (SEQ. ID. 2) that induces freezing or drought
CC   tolerance, operably linked to (c) a non-translated region of a gene
CC   encoding a signal sequence for polyadenylation of mRNA. Also described
CC   are: plant material transformed with DNA comprising fully defined
CC   sequences of 1308 or 816 bp and encoding a transcription regulating
CC   protein or binding protein comprising an AP2 domain amino acid sequence;
CC   a plant tissue comprising plant cells susceptible to infection with
CC   Agrobacterium tumefaciens that contain and express the chimeric gene; and
CC   a method for regulating cold and dehydration regulatory genes in a plant.
CC   The materials are useful in regulating cold and dehydration regulatory
CC   genes in a plant to induce freezing and drought tolerance. This sequence
CC   represents a polynucleotide encoding the putative AP2 domain
CC   transcription factor RAV1 that can be used in the creation of the
CC   chimeric plant-expressible gene of the invention.
XX
SQ   Sequence 1308 BP; 381 A; 226 C; 331 G; 370 T; 0 U; 0 Other;

Query Match   100.0%; Score 1308; DB 12; Length 1308;
Best Local Similarity 100.0%; Pred. No. 1e-300;
Matches 1308;   Conservative 0;   Mismatches 0; Indels   0;   Gaps   0;

Qy   1 GTATACATATACACACATAATTCACAACAACCAACAAACACATTCTGTTTTCTCCATT 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GTATACATATACACACATAATTCACAACAACCAACAAACACATTCTGTTTTCTCCATT 60

Qy   61 GTTTCAAACCATAAAAAAAAACACAGATTAAATGGAATCAGAATGCAGGTTAGCGTTGATGAGAGTAC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTTTCAAACCATAAAAAAAAACACAGATTAAATGGAATCAGAATGCAGGTTAGCGTTGATGAGAGTAC 120

Qy   121 TACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 180

Qy   181 AGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCGT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCGT 240

Qy   241 AGAAGCTGAATCTAGGAGAAGCTTCCGTTCCGTCGTCGTCTCAAAATACAAAGGTGTGTGCCACAACCAAA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AGAAGCTGAATCTAGGAGAAGCTTCCGTTCCGTCGTCGTCTCAAAATACAAAGGTGTGTGCCACAACCAAA 300

Qy   301 CGGAAGAGATGGGGAGCTTCAGATTTACGAGAAACACCACGCGCGTGGCTCGGGACATTCAA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CGGAAGAGATGGGGAGCTTCAGATTTACGAGAAACACCACGCGCGTGGCTCGGGACATTCAA 360

Qy   361 CGAAGAAGACGAAGCCGCTCGTGCCTACGACGTTCCGTTCCGACGTTCCGTCGCCGTGA 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CGAAGAAGACGAAGCCGCTCGTGCCTACGACGTTCCGTTCCACCAGGTTCCGCGCCGTGA 420

Qy   421 CGCCGTCACAAATTTCAAAGACGTGAAGATGACGAAGACGAAGACGAGGTCGATTCTTCGAATTC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CGCCGTCACAAATTTCAAAGACGTGAAGATGACGAAGACGAAGACGAGGTCGATTCTTCGAATTC 480

Qy   481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGA 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGA 540

Qy   541 GCAGAGTAAACCGGCGTCGTAATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGGG 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCAGAGTAAACCGGCGTCGTAATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGGG 600

Qy   601 GTTGAGTAATGATGGTGTTCTACGACGGGTTTAGATCGGCGGAGCACTGTTTGAGAA 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTTGAGTAATGATGGTGTTCTACGACGGGTTTAGATCGGCGGAGCACTGTTTGAGAA 660

Qy   661 AGCGGGTAACGCCAAGCCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGAAACATCACGC 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGCGGGTAACGCCAAGCCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGAAACATCACGC 720

Qy   721 AGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTT 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTT 780

Qy   781 TGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG 840

Qy   841 TTATGTTTGACTAAAGTTGGAGCAGTTCGTTAAGGAGAAGAATCTACGTGCTGGTGA 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTATGTTTGACTAAAGTTGGAGCAGTTCGTTAAGGAGAAGAATCTACGTGCTGGTGA 900

Qy   901 CGTGGTAGTTTCAGTAGATCTAACGGTCAGGATCACACAGTTGTACATTGGGTGGAAGTC 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CGTGGTAGTTTCAGTAGATCTAACGGTCAGGATCACACAGTTGTACATTGGGTGGAAGTC 960

Qy   961 GAGATCCGGGTCAGATTTAGATGCGGCGTCGTAGGAACGACGTCGTTGAACAAAAGAGTGAACGATACTGAGATGTT 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GAGATCCGGGTCAGATTTAGATGCGGCGTCGTAGGAACGACGTCGTTGAACAAAAGAGTGAACGATACTGAGATGTT 1020

Qy   1021 ACCGGAGAGTTCAAGAAACGACGTCGTAGGAGAAACAAAAGAGTGAACAAAGAGTGAACGATACTGAGATGTT 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACCGGAGAGTTCAAGAAACGACGTCGTAGGAGAAACAAAAGAGTGAACAAAGAGTGAACGATACTGAGATGTT 1080

Qy   1081 ATCGTTGGTGTGTAGCAAGAAGCGACGATCTTCAGCGCTCGTAACACTCTTCTTCTT 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTCAGCGCTCGTAACACTCTTCTTCTT 1140

Qy   1141 TTTTTTTTCTTTTGTGTTTAATAATTTTAAAAACTCCATTTTCGTTTTCTTTATTTG 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTTTTTTTCTTTTGTGTTTAATAATTTTAAAAACTCCATTTTCGTTTTCTTTATTTG 1200

Qy   1201 CATCGGTTCTTCTTCTTCTTCTTCTGTTTACCAAAGGTTCATGAGTTGTTTTGTTGTTATTGATGA 1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CATCGGTTCTTCTTCTTCTTCTTCTGTTTACCAAAGGTTCATGAGTTGTTTTGTTGTTATTGATGA 1260

Qy   1261 ACTGTAAATTTATTTATAGGATAAATTTAAAAAGGGTTACTTAGAT 1308
            ||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ACTGTAAATTTATTTATAGGATAAATTTAAAAAGGGTTACTTAGAT 1308

RESULT 2
ABT16588
ID   ABT16588 standard; DNA; 3835 BP.
XX
AC   ABT16588;
XX
DT   03-APR-2003 (first entry)
XX
DE   Ethylene insensitivity related mouse-ear cress DNA SEQ ID No 62.
XX
KW   Mutant; transformed plant; ethylene-response DNA-binding factor; edf1;
KW   edf2; edf3; edf4; fruit; transgenic plant; floral industry;
KW   fruit processing industry; floral senescence; flower longevity;
KW   decreased floral initiation; post-harvest; transportation;
KW   mouse-ear cress; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200289555-A2.
XX
PD   14-NOV-2002.
XX
PF   08-MAY-2002; 2002WO-US014592.
XX
PR   08-MAY-2001; 2001US-0289364P.
PR   08-MAY-2001; 2001US-0289835P.
XX
PA   (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI   Stepanova AN, Ecker JR;
XX
DR   WPI; 2003-120491/11.
XX
PT   Novel mutant or transformed plant comprising mutated forms of edf1, edf2,
PT   edf3 and edf4 genes, and having decreased ethylene sensitivity, such that

PT its fruit ripens more slowly than wild-type version of the plant.
XX
PS Disclosure; Page 80-81; 85pp; English.
XX
CC The invention relates to a mutant or transformed plant comprising mutated
CC forms of ethylene-response DNA-binding factors (edf1), edf2, edf3 and
CC edf4 genes such that the plant exhibits a decreased response to ethylene,
CC and comprises fruit which ripens more slowly than a wild-type version of
CC the plant. The transgenic plants having reduced sensitivity to ethylene
CC are useful for floral industry and fruit processing industries. Since
CC ethylene is involved in floral senescence, the modified plants have
CC longer flower longevity. The modified plants e.g. lettuce, spinach, other
CC leafy vegetables provide higher yields due to decreased floral
CC initiation, since the transformed plants do not bolt or flower easily.
CC The plants provide fruits which ripens more slowly than the wild-type
CC version of the plant, and thus are advantageous in post-harvest and
CC transportation conditions. This polynucleotide represents the DNA of a
CC mouse-ear cress sequence used in the ethylene sensitivity modulation
CC process of the invention
XX
SQ Sequence 3835 BP; 1310 A; 662 C; 677 G; 1186 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1308;   DB 10;   Length 3835;
Best Local Similarity   100.0%;   Pred. No. 1.4e-300;
Matches 1308;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy     1  GTATACATATACACAACTAATTCACAACACAACAACACAACACAACACATTTCTGTTTTCTCCATT    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2410  GTATACATATACACAACTAATTCACAACACAACAACACAACACAACACATTTCTGTTTTCTCCATT  2469

Qy    61  GTTTCAAACCATAAAAAAAAACACAGATTAAATGAATCGAGTAGCGTTGATGAGAGTAC   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2470  GTTTCAAACCATAAAAAAAAACACAGATTAAATGAATCGAGTAGCGTTGATGAGAGTAC  2529

Qy   121  TACAAGTACAGGTTCCATCTGTGAAACCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2530  TACAAGTACAGGTTCCATCTGTGAAACCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT  2589

Qy   181  AGGTAACTTATACAGGATGGGAAGCGGAAGCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCCT   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2590  AGGTAACTTATACAGGATGGGAAGCGGAAGCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCGT  2649

Qy   241  AGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAATACAAAGGTGTGGTGCCACAACCAAA   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2650  AGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAATACAAAGGTGTGGTGCCACAACCAAA  2709

Qy   301  CGGAAGATGGGGAGCTCAGATTACGAGAAACACCAGCGCGTGGGCTCGGGACATTCAA   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2710  CGGAAGATGGGGAGCTCAGATTACGAGAAACACCAGCGCGTGGGCTCGGGACATTCAA  2769

Qy   361  CGAAGAAGACGAAGCGGCCTCGTGCCTACGACGTCGGCGGTTCACAGGTTCCGTCCGCCGTGA   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2770  CGAAGAAGACGAAGCGGCCTCGTGCCTACGACGTCGGCGGTTCACAGGTTCCGTCCGCCGTGA  2829

Qy   421  CGCCGTCACAAATTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATTC   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2830  CGCCGTCACAAATTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATTC  2889

Qy   481  TCATTCGAAATCTGAGATCGTTGATATGTTGAGAGAAATACGAAGAGTTAGA   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2890  TCATTCGAAATCTGAGATCGTTGATATGTTGAGAGAAATACGAAGAGTTAGA  2949

Qy   541  GCAGAGTAAACGGCGTCGTAATGGTAACGAAACATGACTAGGACGTTGTTAACGTCGGG   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2950  GCAGAGTAAACGGCGTCGTAATGGTAACGAAACATGACTAGGACGTTGTTAACGTCGGG  3009

Qy   601  GTTGAGTAATGATGGTGTTCTACGACGGGGTTTAGATCGGCGGAGGCACTGTTTGAGAA   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3010  GTTGAGTAATGATGGTGTTCTACGACGGGGTTTAGATCGGCGGAGGCACTGTTTGAGAA  3069

Qy   661  AGCGGTAAACGGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTTATACCGAAACATCACGC   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3070  AGCGGTAAACGGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTTATACCGAAACATCACGC  3129

Qy   721  AGAGAAACATTTCCGTTACCGTCAAGTAACGTTCCGTGAAGGAGTGTTGTTGAACTT   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3130  AGAGAAACATTTCCGTTACCGTCAAGTAACGTTCCGTGAAGGAGTGTTGTTGAACTT  3189

Qy   781  TGAGGACGTTAACGGGAAAGTGTGGAAAGTGTGGAAGTGGAAGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3190  TGAGGACGTTAACGGGAAAGTGTGGAAAGTGTGGAAGTGGAAGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG  3249

Qy   841  TTATGTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGGAGGAGAATCTACGTGCTGGTGA   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3250  TTATGTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGGAGGAGAATCTACGTGCTGGTGA  3309

Qy   901  CGTGGTTAGTTCAGTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTC   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3310  CGTGGTTAGTTCAGTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTC  3369

Qy   961  GAGATCCGGTCAGATTTGAGATGCGGGTTTGAGATTGTTCGGAGTTAACATTTC  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3370  GAGATCCGGTCAGATTTGAGATGCGGGTTTGAGATTGTTCGGAGTTAACATTTC  3429

Qy  1021  ACCGGAGAGTTCAAGAAACGACCTCGTAGGAAACAAAGAGTGAACGATACTGAGATGTT  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3430  ACCGGAGAGTTCAAGAAACGACGTGTAGGAAACAAAGAGTGAACGATACTGAGATGTT  3489

Qy  1081  ATCGTTGGTGTGTGAGCAAGAAGCAACGCATCTTCACGCCTCGTAACACTCTTCTTCTT  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3490  ATCGTTGGTGTGTGAGCAAGAAGCAACGCATCTTCACGCCTCGTAACACTCTTCTTCTT  3549

Qy  1141  TTTTTTCTTTTGTGTTTAATAATTTTAAAAACTCCATTTCGTTTTCTTTATTTG  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3550  TTTTTTCTTTTGTGTTTAATAATTTTAAAAACTCCATTTCGTTTTCTTTATTTG  3609

Qy  1201  CATCGGTTCTTTCTTCTTGTTTACCAAAGGTTCATGAGTTGTTTTGTGTATTGATGA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3610  CATCGGTTCTTTCTTCTTGTTTACCAAAGGTTCATGAGTTGTTTTGTGTATTGATGA  3669

Qy  1261  ACTGTAAATTTATTTATTATAGGATAAATTTTAAAAAGGGTTACTTAGAT  1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3670  ACTGTAAATTTATTTATTATAGGATAAATTTTAAAAAGGGTTACTTAGAT  3717
```

RESULT 3
AAD05842
ID   AAD05842 standard; cDNA; 1281 BP.
XX
AC   AAD05842;
XX
DT   31-JUL-2001   (first entry)
XX
DE   Arabidopsis thaliana transcription factor G867 cDNA.
XX
PN   WO200136444-A1.
XX
PD   25-MAY-2001.
XX
PF   14-NOV-2000; 2000WO-US031325.
XX
PR   17-NOV-1999;   99US-0166228P.
PR   17-APR-2000;   2000US-0197899P.
PR   22-AUG-2000;   2000US-0227439P.
XX
KW   Transcription factor; trait modification; structural characteristic;
KW   developmental characteristic; gene therapy; agricultural biotechnology;
KW   88.
XX
OS   Arabidopsis thaliana.
XX
FH   Key   Location/Qualifiers
FT   CDS   64..1098
FT   /*tag= a
FT   /product= "Transcription factor G867"
XX

```
PA   (MEND-)  MENDEL BIOTECHNOLOGY INC.
PA   (RIEC/)  RIECHMANN J L.
PA   (REUB/)  REUBER L.
PA   (KEDD/)  KEDDIE J.
PA   (RATC/)  RATCLIFFE O.
PA   (HEAR/)  HEARD J.
PA   (SAMA/)  SAMAHA R.
PA   (YUGG/)  YU G.
PA   (JIAN/)  JIANG C.
XX
PI   Riechmann JL, Reuber L, Keddie J, Ratcliffe O, Heard J, Samaha R;
PI   Yu G, Jiang C;
XX
DR   WPI; 2001-335996/35.
DR   P-PSDB; AAE01964.
XX
PT   Nucleic acids encoding plant transcription factor polypeptides, useful
PT   for altering the developmental and structural characteristics of plants,
PT   e.g. corn, potato and cotton plants.
XX
PS   Claim 4; Page 111-113; 140pp; English.
XX
CC   The present sequence is Arabidopsis thaliana transcription factor G867
CC   cDNA. This sequence is homologous to transcription factor G9. The
CC   transcription factors are used to modify traits associated with
CC   structural or developmental characteristics of plants, e.g.soybean,
CC   wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa,
CC   sugar cane, turf, banana, blackberry, blueberry, strawberry, raspberry,
CC   cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes,
CC   honey dew, lettuce, mango, melon, papaya, peas, watermelon, pineapple,
CC   spinach, squash, sweet corn, tobacco, tomato, peppers, onion, rosaceous
CC   fruits and/or vegetable brassicas when their expression levels are
CC   altered. The manipulation of transcription factor levels in plants offers
CC   great potential in agricultural biotechnology for modifying plant's
CC   traits. The transcription factors are also used in gene therapy
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match            95.9%;  Score 1255;  DB 4;  Length 1281;
Best Local Similarity  99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy         29 CACAACAAACAACATTTCTGTTTCCCATTGTTTCAAACCATAAAAAAAAAAAACACAGAT   88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CACAACAAACAACATTTCTGTTTCCCATTGTTTCAAACCATAAAAAAAAAAAACACAGAT   60

Qy         89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACTACAAGGTTCCATCTGTGAAACC  148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACTACAAGGTTCCATCTGTGAAACC  120

Qy        149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA  208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA  180

Qy        209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCGGCGTAGAAGCTTCCGTCG  268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCGGCGTAGAAGCTTCCGTCG  240

Qy        269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG  328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG  300

Qy        329 AAACACCAGCGCGTGCTGCTCGGGACATTCAACGAAGAACGAAGCCGCCTCGTGCCTAC  388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAACACCAGCGCGTGCTGCTCGGGACATTCAACGAAGAACGAAGCCGCCTCGTGCCTAC  360

Qy        389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG  448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG  420

Qy        449 ATGGACGAAGACGAGTTCGATTTCTCAATTCTTGAATTCTTGAATCTGAAATCTGATATG  508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGACGAAGACGAGTTCGATTTCTCAATTCTTGAATTCTTGAATCTGAAATCTGATATG  480

Qy        509 TTGAGGAAACATACTTATAACGAAGAGTTAGCAGCAGGAGTAAACGGCGTCGTAATGGTAAC  568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGTAGGAAACATACTTATAACGAAGAGTTAGCAGCAGGAGTAAACGGCGTCGTAATGGTAAC  540

Qy        569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAGTAATGATGTGTTCTACGACG  628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAGTAATGATGTGTTCTACGACG  600

Qy        629 GGGTTTAGATGCGCGGAGGCACTGTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG  688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGGTTTAGATGCGCGGAGGCACTGTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG  660

Qy        689 CTAAACCGTTGGTTATACCGGAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT  748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTAAACCGTTGGTTATACCGGAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT  720

Qy        749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  780

Qy        809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG  868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG  840

Qy        869 TTCGTTAAGGAGAAGATCTACGTGCTGGTGACGTGTTGAGTTCAGTTAGTAGATCTAACGGT  928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCGTTAAGGAGAAGATCTACGTGCTGGTGACGTGTTGAGTTCAGTTAGTAGATCTAACGGT  900

Qy        929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  960

Qy        989 CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGGAGTTCAAGAACGACGTCGTA  1048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGGAGTTCAAGAACGACGTCGTA  1020

Qy       1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAGCAACGC  1108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAGCAACGC  1080

Qy       1109 ATCTTTCACGCCTCGTAACAACTCTCTTCTTTTTTTTTTCTTTGTTTGTTTTAATAATT  1168
              ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       1081 ATCTTTCACGCCTCGTAACAACTCTCTTC-TTTTTTTTCTTTGTTTGTTTTAATAATT  1139

Qy       1169 TTTAAAAACTCCATTTTCGTTTTCGTTTTCGTTTTCGTTCTTCTTGTTTACCAA  1228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 TTTAAAAACTCCATTTTCGTTTTCGTTTTCGTTTTCGTTCTTCTTGTTTACCAA  1199

Qy       1229 AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT  1288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT  1259

Qy       1289 TTAAAAA  1295
              |||||||
Db       1260 TTAAAAA  1266
```

RESULT 4
AAD06649
ID   AAD06649 standard; cDNA; 1281 BP.
XX
AC   AAD06649;
XX
DT   10-AUG-2001 (first entry)
XX
DE   A. thaliana transcription factor G867 cDNA.
XX
KW   Plant transcription factor; phenotype; sugar sensing characteristic;
KW   transgenic plant; plant yield; growth; germination; photosynthesis;
KW   glyoxylate metabolism; respiration; pathogen response; wounding response;
KW   cell cycle regulation; pigmentation; flowering; senescence; physiology;
KW   storage organ; metabolism; ss.

```
XX
OS   Arabidopsis thaliana.
XX
FH   Key            Location/Qualifiers
FT   CDS            64..1098
FT                  /*tag= a
FT                  /product= "Transcription factor"
XX
PN   WO200135725-A1.
XX
PD   25-MAY-2001.
XX
PF   14-NOV-2000; 2000WO-US031414.
XX
PR   17-NOV-1999; 99US-0166228P.
PR   17-APR-2000; 2000US-0197899P.
PR   22-AUG-2000; 2000US-0227439P.
XX
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
PA   (JIAN/) JIANG C.
PA   (HEAR/) HEARD J.
PA   (PINE/) PINEDA O.
PA   (PILG/) PILGRIM M.
PA   (ADAM/) ADAM L.
PA   (RIEC/) RIECHMANN J L.
PA   (YUGG/) YU G.
PA   (SAMA/) SAMAHA R.
XX
PI   Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
PI   Yu G, Samaha R;
XX
DR   WPI; 2001-335977/35.
DR   P-PSDB; AAE02548.
XX
PT   Nucleic acids encoding plant transcription factor polypeptides, useful
PT   for altering the sugar sensing characteristics of plants and increasing
PT   yield, e.g. corn, potato and cotton plants.
XX
PS   Claim 4; Page 83-84; 151pp; English.
XX
CC   The patent relates to polynucleotides encoding 35 plant transcription
CC   factors which may be used to modify phenotype associated with a plant's
CC   sugar sensing characteristics and increasing yield when their expression
CC   level is altered. Sugars are central regulatory molecules that control
CC   aspects of physiology, metabolism and development. Therefore the cDNAs
CC   and proteins of the invention are useful for modifying the growth and
CC   germination rates of plants, photosynthesis, glyoxylate metabolism,
CC   respiration, starch and sucrose synthesis and degradation, pathogen
CC   response, wounding response, cell cycle regulation, pigmentation,
CC   flowering and senescence of plants and for modifying sink-source
CC   relationships in seeds, tubers, roots, and other storage organs leading
CC   to an increase in yield. The transcription factor polynucleotides and
CC   polypeptides may be used to alter the structure and developmental
CC   characteristics of plants such as soybean, wheat, corn, potato, cotton,
CC   rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,
CC   blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,
CC   coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,
CC   onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,
CC   tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.
CC   The present sequence is an Arabidopsis thaliana transcription factor cDNA
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match             95.9%;  Score 1255;  DB 5;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;
```

```
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGTTCCATCTGTGAAACC 120
Qy  149 CCGGCGATAACTCCGGCGGAAAAGTCGTCGGTAGTAACTTATACAGGAGGAAGCGGA 208
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CCGGCGATAACTCCGGCGGAAAAGTCGTCGGTAGTAACTTATACAGGAGGAAGCGGA 180
Qy  209 TCAAGCGGTTGTGTTAGATTCAGAGAACCGGCTAGAAGCTGAATCTTAGGAGAGCTTCCGTCG 268
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TCAAGCGGTTGTGTTAGATTCAGAGAACCGGCTAGAAGCTGAATCTTAGGAGAGCTTCCGTCG 240
Qy  269 TCAAAATACAAAGTGTGTGCCACAACCAAACCGGAAGAGTGGGAGCTCAGATTTACGAG 328
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCAAAATACAAAGTGTGTGCCACAACCAAACCGGAAGATGGGAGCTCAGATTTACGAG 300
Qy  329 AAACACCAGCGCCGTGTGGCTCGGGACATTCAACGAAGCAGAAGACCGCTCGTGCCTAC 388
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AAACACCAGCGCCGTGTGGCTCGGGACATTCAACGAAGCAGAAGACCGCTCGTGCCTAC 360
Qy  389 GACGTGCGCGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACAAATTCAAAGACGTGAAG 448
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GACGTGCGCGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACAAATTCAAAGACGTGAAG 420
Qy  449 ATGGACGAAGACGAGGTCGATTCTCATTCGAAATCTGAGAATCGTTGATATG 508
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 ATGGACGAAGACGAGGTCGATTCTCATTCGAAATCTGAGAATCGTTGATATG 480
Qy  509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAGTAAACGGCGTCGTAATGGTAAC 568
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAGTAAACGGCGTCGTAATGGTAAC 540
Qy  569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG 628
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG 600
Qy  629 GGGGTTAGATCGGCGGAGGCACTGTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GGGGTTAGATCGGCGGAGGCACTGTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660
Qy  689 CTAAACCGTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 748
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 CTAAACCGTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 720
Qy  749 AACGTTCCGTGAAAGGAGTGTTGTTGAACTTGAACGGTAACGGAAAGTGTGGAGG 808
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 AACGTTCCGTGAAAGGAGTGTTGTTGAACTTGAACGGTAACGGAAAGTGTGGAGG 780
Qy  809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840
Qy  869 TTCGTTAAGGAGGAAGAATCTACGTGCGTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 TTCGTTAAGGAGGAAGAATCTACGTGCGTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900
Qy  929 CAGGATCAACAGTTGTACATTGGGGTGGAAGTCCGGGTCAGATTTAGATGCGGGT 988
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 CAGGATCAACAGTTGTACATTGGGGTGGAAGTCCGGGTCAGATTTAGATGCGGGT 960
Qy  989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020
Qy 1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTGGTGTGTAGCAAGAAGCAACGC 1108
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTGGTGTGTAGCAAGAAGCAACGC 1080
Qy 1109 ATCTTTCACGCCTCGTAACACTCTTCTTCTTTTTTTTTCTTCTTTTGTTGTTTAATAATT 1168
        |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db 1081 ATCTTTCACGCCTCGTAACACTCTTCTTC--TTTTTTTTCTTCTTTTGTTGTTTAATATT 1139
Qy 1169 TTTAAAAACTTCCATTTTCGTTTTTCGTTTATTTGCATCGGTTTCTTCGTTTGTTTACCAA 1228
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1140 TTTAAAAACTTCCATTTTCGTTTTTCGTTTATTTGCATCGGTTTCTTCGTTTGTTTACCAA 1199
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Qy   29 CACAACAACAAACACATTCGTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 88
        |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db    1 CACAACAACAAACACATTCGTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 60
Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGTTCCATCTGTGAAACC 148
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGTTCCATCTGTGAAACC 120
```

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Qy   1229 AGGTTCATGAGTTGTTTTGTTGTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTGTTGTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
          |||||||
Db   1260 TTAAAAA 1266

RESULT 5
ABK65156
ID   ABK65156 standard; cDNA; 1281 BP.
XX
AC   ABK65156;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Arabidopsis cDNA encoding a transcription factor #8.
XX
KW   Plant; ss; gene; transcription factor; transgenic; agriculture;
KW   metabolic chemical; environmental stress; drought;
KW   microbial disease resistance; herbicide resistance; seed yield;
KW   fruit yield; growth rate; leaf senescence; flower senescence.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200215675-A1.
XX
PD   28-FEB-2002.
XX
PF   22-AUG-2001; 2001WO-US026189.
XX
PR   22-AUG-2000; 2000US-0227439P.
PR   16-NOV-2000; 2000US-00713994.
PR   18-APR-2001; 2001US-00837944.
XX
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
PA   (PILG/) PILGRIM M.
PA   (CREE/) CREELMAN R.
PA   (DUBE/) DUBELL A J.
PA   (HEAR/) HEARD J.
PA   (JIAN/) JIANG C.
PA   (KEDD/) KEDDIE J.
PA   (ADAM/) ADAM L.
PA   (RATC/) RATCLIFF O.
PA   (REUB/) REUBER J L.
PA   (RIEC/) RIECHMANN J L.
PA   (YUGG/) YU G.
PA   (PINE/) PINEDA O.
XX
PI   Pilgrim M, Creelman R, Dubell AJ, Heard J, Jiang C, Keddie J;
PI   Adam L, Ratcliff O, Reuber JL, Riechmann JL, Yu G, Pineda O;
XX
DR   WPI; 2002-292022/33.
DR   P-PSDB; AAU29970.
XX
PT   An isolated or recombinant polynucleotide used to produce a transgenic
PT   plant.
XX
PS   Claim 4; Page 98-100; 941pp; English.
XX
CC   The invention relates to 1 of 232 isolated or recombinant polynucleotides
CC   encoding an Arabidopsis thaliana transcription factor, their variants,
CC   complements, fragments, or related polynucleotide with 31% to 95%
CC   sequence identity, where the plant possesses an altered trait as compared
CC   to a wild-type or reference plant, or the plant exhibits an altered
CC   phenotype as compared to a wild-type or reference plant, or the plant
CC   exhibits ectopic expression or altered expression of one or more genes
CC   associated with a plant trait as compared to a wild plant. Also included
CC   are a transgenic plant comprising the polynucleotides, a computer
CC   readable medium having stored sequence information, and identifying a
CC   homologue sequence from a database comprising a plurality of known plant
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CC   sequences comprising inputting sequence information selected from one of
CC   464 fully defined sequences given in the specification. The isolated or
CC   recombinant polynucleotide is used for producing a plant having a
CC   modified trait, the method comprising selecting a polynucleotide that
CC   encodes a polypeptide or an antisense nucleic acid, inserting the
CC   polynucleotide or antisense nucleic acid into an expression vector,
CC   introducing the vector into a plant or a cell of a plant to overexpress
CC   the polypeptide or antisense nucleic acid, thereby producing a modified
CC   plant, and selecting for a modified trait (e.g. increased production of
CC   agriculturally useful proteins or metabolic chemicals, pest tolerance,
CC   environmental stress response (e.g. drought), microbial disease
CC   resistance, herbicide resistance, seed and fruit yield, growth rate, leaf
CC   and flower senescence and many other traits listed in the specification).
CC   The present sequence is one of the 232 polynucleotides encoding an A.
CC   thaliana transcription factor
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match         95.9%;  Score 1255; DB 6;  Length 1281;
Best Local Similarity 99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  1;

Qy    29 CACAACACAAACACATTTCTGTTTCTCCATTGTTCAAACCATAAAAAAAACACAGAT 88
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CACAACACAAACACATTTCTGTTTCTCCATTGTTCAAACCATAAAAAAAACACAGAT 60

Qy    89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACAGTTCCATCTGTGAAACC 148
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACAGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCCGGA 208
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCCGGA 180

Qy   209 TCAAGCGTTGTGTTAGATTCAGAGAACCGCGTAGAAGCTTAGGAAGCTTCCGTCG 268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTGTTAGATTCAGAGAACCGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGACGGAGGAGTCAGATTTACGAG 328
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGACGGAGGAGTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCGTGTGCTCTGGGACATTCAACGAAGACAGAGACCGCGTCCGTCGCCTAC 388
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCGCGTGTGCTCTGGGACATTCAACGAAGACAGAGACCGCGTCCGTCGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCGCCGTCACAAATTTCAAAGACGTGAAG 448
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAATCGTTGATATG 508
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGGAAACGGTAAACGGCGTCGTAATGGTTAC 568
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGGAAACGGTAAACGGCGACGTTGGGAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy   629 GGGTTAGATCGGCGGAGGCACTGTTGAGAAAGCGGTAACGCGGTTGGGAAG 688
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTAGATCGGCGGAGGCACTGTTGAGAAAGCGGTAACGCGGTTGGGAAG 660

Qy   689 CTAAACCGTTTGGTTATACCGGAAACATCACGAGAAACATTTCCGTTACCGTCAAGT 748
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGGTTATACCGGAAACATCACGAGAGAAACATTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGACGTTAACGGGAAAGTTGGAGG 808
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGACGTTAACGGGAAAGTTGGGAG 780
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Qy   809 TTCCGTTACTCGTATTGAACACAGTAGTCGAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
         ||||||||||||||||| |||||||||| |||||||||||||||| ||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGGAGAATCTACCGTCGTCGGTGGTGACGTGGTTAGTTTCAGTTGAGATCTAACCGT 928
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGGAGAATCTACCGTCGTCGGTGGTGACGTGGTTAGTTTCAGTTGAGATCTAACCGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGCGGT 988
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGCGGT 960

Qy   989 CGGGTTTTGAGATTGTTCGGAGTTAACAATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
         |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy  1049 GGAAACAAAAGAGTGAACGATACGATCTGAGATGTATCGTGGTGTGTAGCAAGAAGCAACGC 1108
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAAGAGTGAACGATACGATACTGAGATGTATCGTGGTGTGTAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTTCACGCCCTCGTAACAACTCCTCTTCTTTTTTTTTTCTTTTGTTCTTTTAATAATT 1168
         ||||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db  1081 ATCTTTCACGCCCTCGTAACAACTCCTCTTC-TTTTTTTTTCTTTTGTTGTTTTAATAATT 1139

Qy  1169 TTTAAAAACTCCATTTTCGTTTTCTTTATTGCATCGGTTTCTTTCTTCTTGTTTACCAA 1228
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAAACTCCATTTTCGTTTTCTTTATTGCATCGGTTTCTTTCTTCTTGTTTACCAA 1199

Qy  1229 AGGTTCATGAGTTGTTTTGTGATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTGTGATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy  1289 TTAAAAA 1295
         |||||||
Db  1260 TTAAAAA 1266
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RESULT 6
ADA15448
ID   ADA15448 standard; DNA; 1281 BP.
XX
AC   ADA15448;
XX
DT   06-NOV-2003 (first entry)
XX
DE   DNA encoding A. thaliana protein, SEQ ID NO:3.
XX
KW   Transgenic plant; plant; transcription factor; trait; root;
KW   plant stability; ds; gene.
XX
OS   Arabidopsis thaliana.
XX
PN   US2003061637-A1.
XX
PD   27-MAR-2003.
XX
PF   21-OCT-2002; 2002US-00278173.
XX
PR   23-MAR-1999; 99US-0125814P.
PR   22-MAR-2000; 2000US-00533393.
XX
PA   (JIAN/) JIANG C.
PA   (BROU/) BROUN P.
PA   (RIEC/) RIECHMANN J L.
PA   (PINE/) PINEDA O.
PA   (ZHAN/) ZHANG J.
PA   (YUGG/) YU G.
PA   (PILG/) PILGRIM M.
PA   (KEDD/) KEDDIE J.
PA   (HEAR/) HEARD J.
PA   (REUB/) REUBER L.
PA   (RATC/) RATCLIFFE O.

PA   (ADAM/) ADAM L.
PA   (SAMA/) SAMAHA R.
XX
PI   Jiang C, Broun P, Riechmann JL, Pineda O, Zhang J, Yu G;
PI   Pilgrim M, Keddie J, Heard J, Reuber L, Ratcliffe O, Adam L;
PI   Samaha R;
XX
DR   WPI; 2003-555503/52.
DR   P-PSDB; ADA15449.
XX
PT   New transgenic plant comprising a recombinant polynucleotide, useful for
PT   altering a plant's trait for increasing plant stability.
XX
PS   Claim 14; SEQ ID NO 3; 159pp; English.
XX
CC   The invention discloses a transgenic plant having an A. thaliana
CC   recombinant polynucleotide (a transcription factor) comprising a sequence
CC   encoding a polypeptide with at least 6 consecutive amino acids of one of
CC   the amino acid sequences given in the specification. The recombinant
CC   polynucleotide alters a trait of the transgenic plant's roots when
CC   compared to the same trait of the roots of another plant lacking the
CC   recombinant polynucleotide. Also claimed are methods for altering the
CC   expression levels of at least one gene of a plant, altering a trait
CC   associated with a plant's roots and altering a plant's trait. The
CC   recombinant polynucleotide further comprises a promoter operably linked
CC   to the nucleotide sequence. The promoter is constitutive or inducible or
CC   root-active. The method for altering a trait associated with roots
CC   comprises transforming a plant with the recombinant polynucleotide,
CC   selecting the transformed plants and identifying a transformed plant with
CC   roots having an altered trait. The method for altering the expression
CC   levels of at least one gene of a plant comprises transforming a plant
CC   with the recombinant polynucleotide and selecting the transformed plant.
CC   The method for altering a trait associated with a plant's roots comprises
CC   transforming a plant with the recombinant polynucleotide and selecting
CC   the transformed plant. The method for altering a plant's trait comprises
CC   providing a database sequence comparing the database sequence with the
CC   polypeptide, selecting the database that meets selected sequence criteria
CC   and transforming the selected database sequence in the plant. The methods
CC   also comprise providing a test polynucleotide, hybridising the test
CC   polynucleotide with the recombinant polynucleotide at low stringency and
CC   transforming the hybridising test polynucleotide in a plant to alter a
CC   trait of the plant. The transgenic plant is useful for altering a plant's
CC   trait for increasing plant stability. The sequence presented is a DNA
CC   encoding a protein of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match   95.9%; Score 1255; DB 9; Length 1281;
Best Local Similarity   99.9%; Pred. No. 4e-288;
Matches 1266; Mismatches   0; Conservative   0; Indels   1; Gaps   1;

```
Qy   29 CACAACCACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 88
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CACAACCACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGGTACAGGTTCCATCTGTGAAACC 148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGGTACAGGTTCCATCTGTGAAACC 120

Qy  149 CCGGGCGATAACTCCCGCGAAAAAGTCGTCGTAGGTAACTTATACAGGATGGGAAGCGGA 208
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CCGGGCGATAACTCCCGCGAAAAAGTCGTCGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy  209 TCAAGCGTTGTTAGATTCAGAGAACGCGCTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TCAAGCGTTGTTAGATTCAGAGAACGCGCTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy  269 TCAAAATACAAAGGTGTGGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAG 328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCAAAATACAAAGGTGTGGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAG 300

Qy  329 AAACACCAGCGCCGTGGCTCGGGACATTCAAGCAGAAGAGACGAAGAAGCCGCTGCCTAC 388
```

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DT    23-SEP-2003 (first entry)
XX
DE    A. thaliana cDNA encoding a disease tolerance transcription factor, G867.
XX
KW    Plant; ss; gene; transcription factor; disease resistance; transgenic;
KW    plant breeding; pathogens resistance; pests; resistance.
XX
OS    Arabidopsis thaliana.
XX
PN    US200304672-A1.
XX
PD    06-MAR-2003.
XX
PF    22-MAR-2000; 2000US-0053302.
XX
PR    22-MAR-2000; 2000US-0053302.
XX
PA    (HEAR/) HEARD J.
PA    (BROU/) BROUN P.
PA    (RIEC/) RIECHMANN J L.
PA    (KEDD/) KEDDIE J.
PA    (PINE/) PINEDA O.
PA    (ADAM/) ADAM L.
PA    (SAMA/) SAMAHA R.
PA    (ZHAN/) ZHANG J.
PA    (YUGG/) YU G.
PA    (RATC/) RATCLIFFE O.
PA    (PILG/) PILGRIM M.
PA    (JIAN/) JIANG C.
PA    (REUB/) REUBER L.
XX
PI    Heard J, Broun P, Riechmann JL, Keddie J, Pineda O, Adam L;
PI    Samaha R, Zhang J, Yu G, Ratcliffe O, Pilgrim M, Jiang C, Reuber L;
XX
DR    WPI; 2003-521768/49.
DR    P-PSDB; AB043125.
XX
PT    New transgenic plants comprising a recombinant gene that alters the
PT    plant's disease tolerance or resistance, useful in plant breeding, e.g.
PT    for generating plants with improved tolerance or resistance to diseases,
PT    pests or pathogens.
XX
PS    Claim 14; Page 64; 124pp; English.
XX
CC    The invention relates to a transgenic plant, comprising a recombinant
CC    polynucleotide that alters the plant's disease tolerance or resistance
CC    when compared with the same trait of another plant lacking the
CC    recombinant polynucleotide. The recombinant polynucleotide comprises a
CC    nucleotide sequence, which encodes a polypeptide comprising at least 6
CC    consecutive amino acids of any of 56 transcription factor proteins
CC    appearing as AB043093-AB043148. Also included are altering the disease
CC    tolerance or resistance of a plant (by: (a) transforming a plant with the
CC    recombinant polynucleotide; (b) selecting the transformed plants; and (c)
CC    identifying a transformed plant with an altered disease tolerance or
CC    resistance), altering the expression levels of at least one gene in a
CC    plant by transforming the plant with the recombinant polynucleotide,
CC    altering a plant's trait (comprising: (a) providing a database sequence;
CC    (b) comparing the database sequence with the polypeptide or
CC    polynucleotide cited above; (c) selecting a database sequence that meets
CC    the selected sequence criteria; and (d) transforming the selected
CC    database sequence in the plant) and altering a plant's trait (comprising:
CC    (a) providing a test polynucleotide; (b) hybridising the test
CC    polynucleotide at low stringency with the recombinant polynucleotide
CC    cited above; and (c) transforming the hybridising test polynucleotide in
CC    a plant to alter a trait of the plant. The transgenic plant is useful in
CC    plant breeding, particularly for generating plants with improved
CC    tolerance or resistance to diseases. The plants have commercial utility
CC    for increasing tolerance or resistance to pathogens and pests. The
CC    present sequence is an Arabidopsis thaliana transcription factor cDNA of
CC    the invention
XX
SQ    Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;
```

```
Db   301 AAACACCAGCGCGTGTGCTCGGACACATTCAACGAAGACGAAGCCGCTCGTGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGCGGTTCACAGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 508
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCTCGTAATGTAAC 568
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCTCGTAATGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAAGTGGTGTTTCTACGACG 628
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAAGTGGTGTTTCTACGACG 600

Qy   629 GGGTTTAGTACGGCGGAGGCACTGTTGTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTTGGTTATACCGAAGATCACGACGAGAAACATTTTCCGTTACCGTCAAGT 748
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGGTTATACCGAAGATCACGACGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTGTTGAACGTTAACGGGAAAGTGTGGAGG 808
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTGTTGAACGTTAACGGGAAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG 868
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCCGGAGTCCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTTGAGATTGTTCGGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy  1049 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTCGGTGGTGTAGCAAGAAGCAACGC 1108
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTCGGTGGTGTAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTTCACGCCTCGTAACAACTCCTTCTTTTTTTTTTTTTTCTTTTGTTGTTTTAATAATT 1168
         ||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1081 ATCTTTCACGCCTCGTAACAACTCCTTCTTC-TTTTTTTTTCTTTTGTTGTTTTAATAATT 1139

Qy  1169 TTTAAAAACTCCATTTCGTTTTCTTTATTTCGTTTCTTTATTTCGTTTCTTGTTTACCAA 1228
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAAACTCCATTTCGTTTTCTTTATTTCGTTTCTTTATTTCGTTTCTTGTTTACCAA 1199

Qy  1229 AGGTTCATGAGTTGTTTTTGTGTTGATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTTGTGTTGATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy  1289 TTAAAAA 1295
         |||||||
Db  1260 TTAAAAA 1266
```

RESULT 7
ACD98391
ID   ACD98391 standard; cDNA; 1281 BP.
XX
AC   ACD98391;
XX

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Query Match          95.9%;  Score 1255;  DB 9;  Length 1281;
Best Local Similarity  99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy    29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 88
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 60

Qy    89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCGGA 208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCGGA 180

Qy   209 TCAAGCGTTGTGTTAGATTCAGAGAACGACGTGAATCTAGGAAGCTTCCGTCG 268
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTGTTAGATTCAGAGAACGACGTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTCGTCTGCGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAG 328
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGGTGTGTGGCTCGGACATTCAACGAAGAAGACGAAGCCCGTCGTGCCTAC 300

Qy   329 AAACACCAGCGCGTGTGGCTCGGACATTCAACGAAGAAGACGAAGCCCGTCGTGCCTAC 388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCGCGTGTGGCTCGGACATTCAACGAAGAAGACGAAGCCCGTCGTGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCGATGATCGTTGATATG 508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCGATGATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy   629 GGGTTTAGATCGGCCGGAGGCACTGTTGTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTTAGATCGGCCGGAGGCACTGTTGTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTTGGTTATACCGAAACATCAGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGGTTATACCGAAACATCAGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGGAGTGTTGTTGAACTTGAGGACGTTAACGGAAGTGTGGAGG 808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGGAGTGTTGTTGAACTTGAGGACGTTAACGGAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAAGTTCAAGAAAACGACGTCGTA 1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAAGTTCAAGAAAACGACGTCGTA 1020

Qy  1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTGTTTTTCTTTTGTTTAATAATT 1168
          ||||||||||||||||||||||||||||| ||||||||| |||||||||||||||||||
Db  1081 ATCTTTCACGCCTCGTAACAACTCTTCTC-TTTTTTTTCTTTTGTTTGTTTAATAATT 1139

Qy  1169 TTTAAAAACTCCATTTCGTTTCTTATTGCATCGGTTTCTTCTTCTTGTTTACCAA 1228
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAAACTCCATTTCGTTTCTTATTGCATCGGTTTCTTCTTCTTGTTTACCAA 1199

Qy  1229 AGGTTCATGAGTTGTTTTTGTTGTTATTGAATGAACGTAAAATTTATTTATTAGGATAAATT 1288
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTTGTTGTTATTGAATGAACGTAAAATTTATTTATTAGGATAAATT 1259

Qy  1289 TTAAAAA 1295
          |||||||
Db  1260 TTAAAAA 1266
```

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RESULT 8
ADB31784
ID   ADB31784 standard; DNA; 1281 BP.
XX
AC   ADB31784;
XX
DT   04-DEC-2003  (first entry)
XX
DE   DNA encoding plant (A. thaliana) transcription factor polypeptide #9.
XX
KW   Plant; transcription factor; transgenic plant; transgenic; plant trait;
KW   modified trait; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   US2003101481-A1.
XX
PD   29-MAY-2003.
XX
PF   15-NOV-2002; 2002US-00295403.
XX
PR   22-SEP-1998;   98US-0101349P.
PR   06-OCT-1998;   98US-0103312P.
PR   17-NOV-1998;   98US-0108734P.
PR   22-DEC-1998;   98US-0113409P.
PR   13-SEP-1999;   99US-00394519.
XX
PA   (ZHAN/)  ZHANG J.
PA   (FROM/)  FROMM M.
PA   (HEAR/)  HEARD J.
PA   (RIEC/)  RIECHMANN J L.
PA   (ADAM/)  ADAM L.
PA   (BROU/)  BROUN P.
PA   (PINE/)  PINEDA O.
PA   (REUB/)  REUBER L.
PA   (KEDD/)  KEDDIE J.
PA   (YUGG/)  YU G.
PA   (JIAN/)  JIANG C.
XX
PI   Zhang J, Fromm M, Heard J, Riechmann JL, Adam L, Broun P;
PI   Pineda O, Reuber L, Keddie J, Yu G, Jiang C;
XX
DR   WPI; 2003-597572/56.
DR   P-PSDB; ADB31785.
XX
PT   New isolated polypeptides and polynucleotide sequences, useful for
PT   screening a molecule to identify a molecule that modifies plant trait,
PT   and for producing plants with modified traits.
XX
PS   Claim 1; SEQ ID NO 17; 17pp; English.
XX
CC   The present invention relates to the isolation of plant (Arabidopsis
CC   thaliana) transcription factor polypeptide and polynucleotide sequences.
```

CC   Also disclosed are: an expression vector comprising the isolated
CC   polynucleotide, a host cell comprising the expression vector, a
CC   transgenic plant comprising the isolated polynucleotide, a transgenic
CC   plant ectopically expressing the isolated polynucleotide or polypeptide,
CC   a method for screening a molecule to identify a molecule that modifies a
CC   plant trait by placing the molecule in contact with the plant, and
CC   monitoring the effect of the molecule on the expressing or activity of
CC   the polypeptide or polynucleotide, and producing a transgenic plant
CC   having a modified trait by ectopically expressing the isolated
CC   polypeptide and selecting a plant with the modified trait. The
CC   polypeptides, polynucleotides and methods are useful for screening a
CC   molecule to identify a molecule that modifies plant trait, and for
CC   producing plants with modified traits. The present sequence represents a
CC   plant transcription factor polynucleotide of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the
CC   USPTO web site at seqdata.uspto.gov.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match   95.9%; Score 1255; DB 10; Length 1281;
Best Local Similarity   99.9%; Pred. No. 4e-288;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

Qy   29 CACAACACAAACACATTCTCGTTCTCCATTGTTCCAAACCATAAAAAAAAACACAGAT 88
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CACAACACAAACACATTCTCGTTCTCCATTGTTCCAAACCATAAAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACACAGGTTCCATCTGTGAAACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACACAGGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy   209 TCAAGCGGTTGTGTTGATTCAGAGAACGCGTGAATCTAGGAAGCTTCCGTCG 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGGTTGTGTTGATTCAGAGAACGCGTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGACGAAGCCGCTCGTGCCTAC 388
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGACGAAGCCGCTCGTGCCTAC 360

Qy   389 GAGTCGCGGTCACAGGTTCCGTCCGCGTGACGCCGTGCACAAATTTCAAAGACGTGAAG 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGTCGCGGTCACAGGTTCCGTCCGCGTGACGCCGTGCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGGTCGATTCTTGAATTCATTCCGAAATCTGAGATCGTTGATATG 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAAGACGAGGTCGATTCTTGAATTCATTCCGAAATCTGAGATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGACGAGTAAACGGCGTCGTAATGGTAAC 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGACGAGTAAACGGCGTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTGTGTTTCTACGACG 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTGTGTTTCTACGACG 600

Qy   629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTTAACGCCAAGCGACGTTGGGAAG 688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTTAACGCCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTTGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGTAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGTAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGCGTGAGTTTCAGTAGATCTAACGT 928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGCGTGAGTTTCAGTAGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGCTCGTA 1048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1108
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTCTTTTGTTGTTTAATAATT 1168
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTTCTTTTGTTGTTTAATAATT 1139

Qy   1169 TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGGTTCTTCTTTGTTTGTTTACCAA 1228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGGTTCTTCTTTGTTTGTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
              |||||||
Db   1260 TTAAAAA 1266

RESULT 9
ADD55665
ID   ADD55665 standard; cDNA; 1281 BP.
XX
AC   ADD55665;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Thalecress environmental stress-related cDNA #12.
XX
KW   Thalecress; environmental stress; ss; gene; plant; viral infection;
KW   fungal infection; microbial infection; herbicide resistance; heat; cold;
KW   heavy metal; low light; drought; osmotic stress; salt concentration;
KW   transgenic.
XX
OS   Arabidopsis thaliana.
XX
PN   US2003131386-A1.
XX
PD   10-JUL-2003.
XX
PF   22-OCT-2002; 2002US-00278536.
XX
PR   23-MAR-1999; 99US-0125814P.
PR   22-MAR-2000; 2000US-00532591.
XX
PA   (SAMA/) SAMAHA R.
PA   (HEAR/) HEARD J.
PA   (JIAN/) JIANG C.
PA   (PINE/) PINEDA O.
PA   (REUB/) REUBER L.
PA   (RIEC/) RIECHMANN J L.
PA   (YUGG/) YU G.

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PA   (KEDD/)  KEDDIE J.
PA   (RATC/)  RATCLIFFE O.
PA   (PILG/)  PILGRIM M.
PA   (ADAM/)  ADAM L.
PA   (BROU/)  BROUN P.
XX
PA   (ZHAN/)  ZHANG J.
XX
PI   Samaha R, Heard J, Jiang C, Pineda O, Reuber L, Riechmann JL;
PI   Yu G, Keddie J, Ratcliffe O, Pilgrim M, Adam L, Broun P, Zhang J;
XX
DR   WPI; 2003-829608/77.
DR   P-PSDB; ADD55666.
XX
PT   New recombinant polynucleotide for altering the regulation of gene
PT   expression of plants to modify the plant's traits, particularly the
PT   plant's environmental stress tolerance.
XX
PS   Claim 14; SEQ ID NO 23; 219pp; English.
XX
CC   The invention relates to a recombinant polynucleotide that alters a
CC   plant's environmental stress tolerance when compared with the same trait
CC   of another plant lacking the recombinant polynucleotide. Also included
CC   are a transgenic plant comprising the novel recombinant polynucleotide
CC   having a sequence that encodes a polypeptide comprising at least 6
CC   consecutive amino acids of any of the 55 250-500 residue amino acid
CC   sequences (S1), given in the specification, altering the environmental
CC   stress response or tolerance of a plant, or altering a plant's trait and
CC   altering the expression levels of at least one gene in a plant. The
CC   recombinant polynucleotide and methods are useful for altering the
CC   regulation of gene expression of plants to modify the plant's traits, in
CC   particular with respect to environmental stress responses (e.g. to viral
CC   infection, fungal infection, microbial infection, herbicide resistance,
CC   heat, cold, heavy metals, low light, drought, osmotic stress and salt
CC   concentration). The present sequence is an environmental stress related
CC   polynucleotide of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match            95.9%;  Score 1255;  DB 10;  Length 1281;
Best Local Similarity  99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;

Qy    29 CACAACAAAACACATTCGTTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 88
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CACAACAAAACACATTCGTTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 60

Qy    89 TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACACAAGGTTCCATCTGTGAAACC 148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACACAAGGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCCGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCCGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy   209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAGAGCTTCCGTCG 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAGAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACCAAACGGAAGATGGGAGCTTCAGATTTACGAG 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACCAAACGGAAGATGGGAGCTTCAGATTTACGAG 300

Qy   329 AAACACCAGCCGCGTGTGGCTCGGGACATTCAACGAAGACGAAGAGACGAGCCGGTCGTCGCCTAC 388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCCGCGTGTGGCTCGGGACATTCAACGAAGACGAAGAGACGAGCCGGTCGTCGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGGTTCGGTCGGTCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGCGGTTCACAGGTTCGGTCGGTCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGCGAGGTCGATTCTCATTCGAAATCTGAAATCTGAGATCGTTGATATG 508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAAGACGAGCGAGGTCGATTCTCATTCGAAATCTGAAATCTGAGATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAATGGTAAC 568
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACG 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACG 600

Qy   629 GGGTTAGATCGGCGGAGGCACTGTTGAAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTAGATCGGCGGAGGCACTGTTGAAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGGAGTGTTGTTGAACTTGAGGACGTTAACGGAGGAAAGTGTGGAGG 808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGGAGTGTTGTTGAACTTGAGGACGTTAACGGAGGAAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGAGCAGG 868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGAGCAGG 840

Qy   869 TTCGTTAAGGAGAAGAATCTACGTGCTCGTGGTGTAGTTTCAGTAGATCGTAACGGT 928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGAAGAATCTACGTGCTCGTGGTGTAGTTTCAGTAGATCGTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGAGTGGAAGTCGAGATCCGGTCAGATTTAGATGCGGGT 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGAGTGGAAGTCGAGATCCGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy  1049 GGAACAAAAGAGTGAACGATACTGAGATGTATCGTTGGTGAGCAAGAAGCAACGC 1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAACAAAAGAGTGAACGATACTGAGATGTATCGTTGGTGAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTTCACGCCTCGAACAACTCTTCTTTCTTATTTGCATCGGTTCTTCTTTGTTTACCAA 1168
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  1081 ATCTTTCACGCCTCGAACAACTCTTCTTTC-TTTTTTTCTTATTTGCATCGGTTCTTCTTTGTTTACCAA 1139

Qy  1169 TTTAAAAACTCCATTTCGTTTTCTTATTTGCATCGTTTCTTCTTCGTGTTTTACCAA 1228
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAAACTCCATTTCGTTTTCTTATTTGCATCGTTTCTTCTTCGTGTTTTACCAA 1199

Qy  1229 AGGTTCATGAGTTGTTTTGTTGTATTGAAGACTGTAAATTTATTTATTTATAGGATAAATT 1288
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTGTTGTATTGAAGACTGTAAATTTATTTATTTATAGGATAAATT 1259

Qy  1289 TTAAAAA 1295
          |||||||
Db  1260 TTAAAAA 1266

RESULT 10
ADD30762
ID   ADD30762 standard; cDNA; 1281 BP.
XX
AC   ADD30762;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Plant yield-related polynucleotide clone G867.
XX
KW   ds; transcription factor; transgenic plant; growth rate; senescence;
KW   seed germination rate; plant vigor; seedling vigor.
XX
OS   Arabidopsis thaliana.
XX
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PN   WO2003013227-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-US025805.
XX
PR   09-AUG-2001; 2001US-0310847P.
PR   19-NOV-2001; 2001US-0336049P.
PR   11-DEC-2001; 2001US-0338692P.
PR   14-JUN-2002; 2002US-0171468.
XX
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI   Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE;
PI   Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;
PI   Broun PE;
XX
DR   WPI; 2003-248221/24.
DR   P-PSDB; ADD30763.
XX
PT   New plant transcription factor polynucleotides and polypeptides, useful
PT   in producing transgenic plants with commercially valuable properties,
PT   such as an alteration in a plant growth characteristic, e.g. growth rate
PT   or apomixis.
XX
PS   Disclosure; SEQ ID NO 791; 454pp; English.
XX
CC   The invention relates to a number of isolated Arabidopsis thaliana cDNA
CC   sequences and their encoded proteins which are especially transcription
CC   factor related cDNA's and proteins. The isolated or recombinant plant
CC   transcription factor polynucleotides and polypeptides are useful in
CC   producing transgenic plants with commercially valuable properties, i.e.
CC   modified or altered desirable traits as compared to a reference plant,
CC   such as an alteration in a plant growth characteristic, e.g. growth rate,
CC   germination rate of seeds, vigor of plants and seedlings, or leaf and
CC   flower senescence. Sequence information related to the polynucleotides
CC   and polypeptides can also be used in bioinformatic search methods. The
CC   transgenic plant is useful for growing a progeny plant from a parent
CC   plant. This sequence represents one of the cDNAs of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match             95.9%;  Score 1255;  DB 10;  Length 1281;
Best Local Similarity   99.9%;
Matches 1266;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;

Qy     29 CACACACAAACACATTTCGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 88
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACACACAAACACATTTCGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 60

Qy     89 TAAATGGAATCGAGTAGGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCGTGAAACC 148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TAAATGGAATCGAGTAGGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCGTGAAACC 120

Qy    149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGGCGGA 208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGGCGGA 180

Qy    209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTGAGAAGCTTCCGTCG 268
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTGAGAAGCTTCCGTCG 240

Qy    269 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGTCAGATTTACGAG 328
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGTCAGATTTACGAG 300

Qy    329 AAACACCAGCGCGTGTGGCTCGGCGACATTCAACGAAGAAGACCGCTCGTGCCTAC 388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAACACCAGCGCGTGTGGCTCGGCGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 360

Qy    389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTCGACGCCCGTCGACGACGTGAAG 448
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGTCGCGGTTCACAGGTTCCGTCGCGCCCTGACGCCCGTCGACGACGTGAAG 420
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```
Qy    449 ATGGACGAAGACGAGGTCGATTTCTTCATTCGTGAAATCTGAGATCGTTGATATG 508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGGACGAAGACGAGGTCGATTTCTTCATTCGTGAAATCTGAGATCGTTGATATG 480

Qy    509 TTGAGGAAACATACTTATATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTGAGGAAACATACTTATATAACGAAGAGTTAGACGAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy    569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTGAGTAATGATGGTGTTTCTACGACG 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy    629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy    689 CTAAACCGTTGTTATACCGGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 748
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTAAACCGTTGTTATACCGGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 720

Qy    749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAG 808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAG 780

Qy    809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy    869 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTGAGTTCAGTAGATCTAACGGT 928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTGAGTTCAGTAGATCTAACGGT 900

Qy    929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy    989 CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTCTTTTGTTTGTTTTAATAATT 1168
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTCTTTTGTTTGTTTTAATAATT 1139

Qy   1169 TTTAAAAACTCCATTTTCGTTTTCGTTTTCTTTTATTTGCATCGGTTTCTTCTTCTTGTTTTACCAA 1228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 TTTAAAAACTCCATTTTCGTTTTCTTTTATTTGCATCGGTTTCTTCTTCTTGTTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTTGTTTGTGTTGTTATTGATGAACTGTAAATTTATTTATTAGGATAAATT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTTGTTTGTGTTATTGATGAACTGTAAATTTATTTATTAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
          ||||||
Db   1260 TTAAAAA 1266
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RESULT 11
ADE37198
ID   ADE37198 standard; cDNA; 1281 BP.
XX
AC   ADE37198;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Plant yield related polynucleotide clone G867.
XX
KW   ds; gene; transcription factor; tolerance; environmental condition;
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KW   microbial disease; fungal disease; viral disease; pest infestation;
KW   herbicide sensitivity; heavy metal tolerance; heavy metal uptake;
KW   growth improvement; photocondition; nutrient uptake; hormone sensitivity;
KW   transgenic plant.
XX
OS   Arabidopsis thaliana.
XX
FH   Key            Location/Qualifiers
FT   CDS            64..1098
FT                  /*tag= a
FT                  /product= "transcription factor"
XX
PN   WO2003014327-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-US026966.
XX
PR   09-AUG-2001; 2001US-0310847P.
PR   19-NOV-2001; 2001US-0336049P.
PR   11-DEC-2001; 2001US-0338692P.
PR   14-JUN-2002; 2002US-00171468.
XX
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI   Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN;
PI   Ratcliffe O, Pineda O, Yu GL, Broun PB;
XX
DR   WPI; 2003-256576/25.
DR   P-PSDB; ADB37199.
XX
PT   New stress-related transcription factor polynucleotides and polypeptides,
PT   useful for producing transgenic plants with e.g. improved tolerance to
PT   diseases or pests, decreased herbicide sensitivity, or improved nutrient
PT   uptake.
XX
PS   Disclosure; SEQ ID NO 137; 470pp; English.
XX
CC   The invention relates to a number of cDNA sequence and their encoded
CC   proteins which are especially transcription factor cDNAs and their
CC   proteins. The isolated or recombinant polynucleotide is useful for
CC   producing a modified plant with a modified trait, e.g. enhanced tolerance
CC   to environmental conditions, improved tolerance to microbial, fungal or
CC   viral diseases, improved tolerance to pest infestation, decreased
CC   herbicide sensitivity, improved tolerance of heavy metals, or enhanced
CC   ability to take up heavy metals, improved growth under poor
CC   photoconditions, improved nutrient uptake, or reduced hormone
CC   sensitivity. The transgenic plants are useful for growing a progeny plant
CC   comprising the desired trait. The polynucleotides and polypeptides are
CC   also useful in bioinformatic search methods. This sequence represents one
CC   of the cDNAs of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match      95.9%;   Score 1255;   DB 10;   Length 1281;
Best Local Similarity  99.9%;   Pred. No. 4e-288;
Matches 1266;   Conservative  0;   Mismatches  0;   Indels  1;   Gaps  1;

Qy      29  CACAACACAAAACACATTTCGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAAACACAGAT    88
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  CACAACACAAAACACATTTCGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAAACACAGAT    60

Qy      89  TAAATGGAATCGAGTAGCGTTGATGAGTACTACAAGTAACTTATACAGGATGGGAAGACCGGA   148
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  TAAATGGAATCGAGTAGCGTTGATGAGTACTACAAGTAACTTATACAGGATGGGAAGACC   120

Qy     149  CCGGCGATAACTCCGGCGAAAAAGTCGTCGTAGTAACTCGTCGTAGTAGAAGCTGAATCCGTCG   208
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  CCGGCGATAACTCCGGCGAAAAAGTCGTCGTAGTAACTCGTCGTAGTAGAAGCTGAATCCGTCG   180

Qy     209  TCAAGCGTTGTGTTAGATTCAGAGAACGCGCTAGAAGCTGAATCCGTAGATTCAGAGAAGCTTCCGTCG   268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  TCAAGCGTTGTGTTAGATTCAGAGAACGCGCTAGAAGCTGAATCCGTAGATTCAGAGAAGCTTCCGTCG   240
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Qy     269  TCAAAATACAAAGGTGTGGTGCGCACCACCAAACGCGAGATGGGAGCTCAGATTTACGAG   328
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  TCAAAATACAAAGGTGTGGTGCCACACCAAACGCGAGATGGGAGCTCAGATTTACGAG   300

Qy     329  AACACCAGCGCGTGCGTGCTCGGGACATTCAACGAAGAAGAGCAAGCCGCTCGTCGTGCCTAC   388
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  AACACCAGCGCGTGCGTGCTCGGGACATTCAACGAAGAAGAGCAAGCCGCTCGTCGTGCCTAC   360

Qy     389  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG   448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG   420

Qy     449  ATGGACGAAGAAGAAGAGGTCGATTTCTTCATTCGAAATTCTCATTCGAAATCTGAGATCGTGATATG   508
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  ATGGACGAAGAAGAAGAGGTCGATTTCTTCATTCGAAATTCTCATTCGAAATCTGAGATCGTGATATG   480

Qy     509  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACCGCGTCGTAATGGTAAC   568
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACCGGTCGTCGTAATGGTAAC   540

Qy     569  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG   628
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG   600

Qy     629  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGGACGTTGGGAGG   688
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGGACGTTGGGAGG   660

Qy     689  CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTTACCGTCAAGT   748
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTTACCGTCAAGT   720

Qy     749  AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGGGAGG   808
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGGGAGG   780

Qy     809  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG   868
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG   840

Qy     869  TTCGTTAAGGAGAGAATCTACGTGCTCGGTGACGTGGTTAGTTTCAGTGATCTAACGGT   928
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  TTCGTTAAGGAGAGAATCTACGTGCTCGGTGACGTGGTTAGTTTCAGTGATCTAACGGT   900

Qy     929  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT   988
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATCGGGGT   960

Qy     989  CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA   1048
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA   1020

Qy    1049  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTGTGTAGCAAGAAGCAACGC   1108
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTGTGTAGCAAGAAGCAACGC   1080

Qy    1109  ATCTTTCACGCCTCGTAACAACCTTCTTCTTCTTC-TTTTTTTTTGTTTGTTTAATAATT   1168
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    1081  ATCTTTCACGCCTCGTAACAACACTCCTCTTCTTCTTTTTTTTTGTTTGTTTAATAATT   1139

Qy    1169  TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGGTTTCTTCTTTCTTCTTGTTTTACCAA   1228
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140  TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGGTTTCTTCTTTCTTCTTGTTTTACCAA   1199

Qy    1229  AGGTTCATGAGTTGTTTTTGTTATTGATGAACTGTAAATTTATTTATTAGGATAAATT   1288
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200  AGGTTCATGAGTTGTTTTTGTTATTGATGAACTGTAAATTTATTTATTAGGATAAATT   1259

Qy    1289  TTAAAAA   1295
            |||||||
Db    1260  TTAAAAA   1266
```

```
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy    29  CACAACAACAAACACATTCTGTTTCTCCATTGTTTCAAACCATAAAAAAACCATAAAAAAAAACACAGAT   88
          |||||||||||||||||||||||||||||||||||||||||||||||||          |||||||||||
Db     1  CACAACAACAAACACATTCTGTTTCTCCATTGTTTCAAACCATAAAAAAACCATAAAAAAAAACACAGAT   60

Qy    89  TAAATGAATCGAGTAGCGTTGATGAGAGTACTACAGTACACAGGTTCCATCTGTGAAACC              148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TAAATGAATCGAGTAGCGTTGATGAGAGTACTACAGTACACAGGTTCCATCTGTGAAACC              120

Qy   149  CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA              208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA              180

Qy   209  TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTAGAAGTTCCGTCG                      268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTAGAAGTTCCGTCG                      240

Qy   269  TCAAAATACAAAGGTGGTGCCACAACCAAACGGAGAATGGGAGCTCAGATTACGAG                   328
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TCAAAATACAAAGGTGGTGCCACAACCAAACGGAGAATGGGAGCTCAGATTACGAG                   300

Qy   329  AAACACCAGCGCGTGTGGCTCCGGACATTCAACGAGAAGAAGACGAAGCCGCCGTCGCCTAC             388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AAACACCAGCGCGTGTGGCTCCGGACATTCAACGAGAAGAAGACGAAGCCGCCGTCGCCTAC             360

Qy   389  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCCGTCACAAATTCAAAGACGTGAAG               448
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCCGTCACAAATTCAAAGACGTGAAG               420

Qy   449  ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAGAATCTGATTCGTGATATG                508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAGAATCTGATTCGTGATATG                480

Qy   509  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGCAGAGTAAACGGCTCGTAATGGTAAC             568
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGCAGAGTAAACGGCTCGTAATGGTAAC             540

Qy   569  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGACTAATGATGTGTTTCTACGACG                628
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGACTAATGATGTGTTTCTACGACG                600

Qy   629  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG                688
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG                660

Qy   689  CTAAACCGTTTGGTTATACCGGAGAACATCAGCAGAGAAACATTTTCCGTTACCGTCAAGT              748
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CTAAACCGTTTGGTTATACCGGAGAACATCAGCAGAGAAACATTTTCCGTTACCGTCAAGT              720

Qy   749  AACGTTTCCGTGAAAGGAGTGTGTTGAACTTGAGGACGTTAACGGAAAGTGTGGAGG                  808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AACGTTTCCGTGAAAGGAGTGTGTTGAACTTGAGGACGTTAACGGAAAGTGTGGAGG                  780

Qy   809  TTCCGGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG              868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TTCCGGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG              840

Qy   869  TTCGTTAAGGAGAAGAATCTACGTGCTGGTGGACGTGGTTAGTTTCAGTTGGATCTAACGT              928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  TTCGTTAAGGAGAAGAATCTACGTGCTGGTGGACGTGGTTAGTTTCAGTTGGATCTAACGT              900

Qy   929  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAAAGGTTCGGAGCAGG               988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAAAGGTTCGGAGCAGG               960

Qy   989  CGGGTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGACTCGTA              1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  CGGGTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGACTCGTA              1020

Qy  1049  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAGCAACGC                   1108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAGCAACGC                   1080
```

RESULT 12

AAD47502

ID   AAD47502 standard; DNA; 1281 BP.

XX

AC   AAD47502;

XX

DT   24-FEB-2003 (first entry)

XX

DE   Arabidopsis thaliana G867 transcription factor DNA.

XX

KW   Transcription factor; metabolite pathway; terpenoid; limonene synthase;
KW   alkaloid pathway gene; taxadiene synthase; biological pathway; freezing;
KW   abiotic stress; cold; drought; heat; nutrient deficiency; biotic stress;
KW   infection; developmental pathway; flowering; root development; TDS; LS;
KW   transgenic; transgenic plant; gene; ds.

XX

OS   Arabidopsis thaliana.

XX

FH   Key   Location/Qualifiers
CDS
FT   64..1098
FT   /*tag= a
FT   /product= "Arabidopsis thaliana G867 transcription factor
FT   protein"

XX

PN   WO200274917-A2.

XX

PD   26-SEP-2002.

XX

PF   15-MAR-2002; 2002WO-US007999.

XX

PR   16-MAR-2001; 2001US-00810836.

XX

PA   (MEND-) MENDEL BIOTECHNOLOGY INC.

XX

PI   Broun P;

XX

DR   WPI; 2003-018799/01.
DR   P-PSDB; AAE30051.

XX

PT   Determining whether one of several test transcription factor (TF)
PT   polynucleotides encodes pathway TF by determining expression from pathway
PT   gene promoter linked to reporter gene in a cell in presence of test
PT   polynucleotides.

XX

PS   Disclosure; Page 162-163; 221pp; English.

XX

CC   The present invention relates to a high-throughput method for identifying
CC   a polynucleotide which encodes a transcription factor for controlling the
CC   expression of one or more genes in a pathway. The method is useful for
CC   determining whether a member of a pool of test transcription factor or a
CC   polynucleotides encodes a biosynthetic pathway transcription factor or a
CC   primary metabolite pathway gene or a secondary metabolite pathway gene
CC   such as a terpenoid or alkaloid pathway gene transcription factor. It is
CC   also useful for determining whether a member of a pool of test encodes a
CC   Mentha sp. or Taxus sp. terpenoid pathway gene where the terpenoid
CC   pathway gene encodes limonene synthase (LS) or taxadiene synthase (TDS).
CC   It is also useful for identifying one or more transcription factors that
CC   activate one or more genes of a biological pathway of a plant, fungi or
CC   animal cell, where the biological pathway can be a biochemical pathways
CC   such as biosynthetic pathways for soluble and insoluble carbohydrates,
CC   for amino acids and a response pathway to abiotic stress such as cold,
CC   freezing, drought, heat, nutrient deficiency, pH or biotic stress such as
CC   fungal, viral or bacterial infection, developmental pathway such as
CC   flowering, root development, a response pathway to environmental cues
CC   such as light intensity and light quality, circadian rhythm. Sequences of
CC   the invention are used to generate transgenic plants. The present
CC   sequence is Arabidopsis thaliana G867 transcription factor DNA

XX

SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

XX

Query Match   95.9%;   Score 1255;   DB 10;   Length 1281;
Best Local Similarity 99.9%;   Pred. No. 4e-288;

PT

XX

PS Claim 1; SEQ ID NO 169; 435pp; English.

XX

CC The invention describes a transgenic plant comprising a recombinant
CC polynucleotide of any one of more than 500 nucleotide sequences fully
CC defined in the specification or its complement. The method of the
CC invention can be used to produced a plant having altered traits such as:
CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
CC sensitivity; disease resistance; sugar sensing; early or late flowering;
CC altered flower structure, change in stem bifurcations, altered branching
CC pattern, reduced apical dominance, reduced trichome density; lack of
CC trichomes; reduced ectopic trichome development; altered trichome
CC development; increase in trichome number; altered stem morphology;
CC increased root growth; increased root hairs; altered seed development;
CC altered cell proliferation or cell differentiation; rapid development;
CC premature senescence; increased necrosis; increase in seedling or plant
CC size; decreased plant size; leaf morphology; seed morphology; seed
CC biochemistry; increase in root anthocyanins; increase in plant
CC anthocyanins, or alteration in light response or shade avoidance. The
CC transgenic plant, polynucleotides and polypeptides are useful in
CC bioinformatic search methods. This sequence encodes a plant transcription
CC factor that can be used in the creation of a transgenic plant with
CC altered traits.

XX

SQ Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match   95.9%; Score 1255; DB 12; Length 1281;
Best Local Similarity 99.9%; Pred. No. 4e-288;
Matches 1266; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      29 CACAACACAAACACATTCTGTTTCTCCATTGTTCAAACCATAAAAAACACAGAT 88
           ||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1 CACAACACAAACACATTCTGTTTCTCCATTGTTCAAACCATAAAAAAACACAGAT 60

Qy      89 TAAATGGAATGAGTAGCGTTGATGAGAGTACTACAAGTACTACAAGTTCCATCTGTGAAACC 148
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TAAATGGAATGAGTAGCGTTGATGAGAGTACTACAAGTACTACAAGTTCCATCTGTGAAACC 120

Qy     149 CCGGCGGATAACTCCGGCGGAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGA 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCGGCGGATAACTCCGGCGGAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGA 180

Qy     209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy     269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 328
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 300

Qy     329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAAGACGAGCCGCTCGTCGCCTAC 388
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAAGACGAGCCGCTCGTCGCCTAC 360

Qy     389 GACGTCGCGTTCACAGGTTCCGTCGCCGTGACCCGTCACAAATTTCAAAGACGTGAAG 448
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACGTCGCGTTCACAGGTTCCGTCGCCGTGACCCGTCACAAATTTCAAAGACGTGAAG 420

Qy     449 ATGGACGAAGACAGAGCGAGTCGATTTCTCATTCGAAATCTGAATCTGAGATCGTTGATATG 508
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ATGGACGAAGACAGAGCGAGTCGATTTCTCATTCGAAATCTGAATCTGAGATCGTTGATATG 480

Qy     509 TTGAGGAAACATACTTATAACGGACGTTAGAGCAGAGTAAACGGTAATGTAAC 568
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTGAGGAAACATACTTATAACGGACGTTAGAGCAGAGTAAACGGTAATGTAAC 540

Qy     569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy     629 GGGTTTAGATCGGCCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAAG 688
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 1109 ATCTTTCACGCCGTAACAACCTCTTCTCTTTTTTTTTCTTTGTGTGTTTAATAATT 1168
           ||||||||||||||||||||||||||||| |||||||| |||||||||||||||||
Db 1081 ATCTTTCACGCCGTAACAACCTCTTCTCTC-TTTTTTTCTTTGTGTGTTTAATAATT 1139

Qy 1169 TTTAAAAACTCATTTCGTTTCTTATTGCATCGGTTCCTTCTTCTTGTTTACCAA 1228
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1140 TTTAAAAACTCCATTTCGTTTCTTATTGCATCGGTTCCTTCTTCTTGTTTACCAA 1199

Qy 1229 AGGTTCATGAGTTGTTTTTGTGTATGAACTGTAAATTTTATTTATAGGATAAATT 1288
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1200 AGGTTCATGAGTTGTTTTTGTGTATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy 1289 TTAAAAA 1295
          |||||||
Db 1260 TTAAAAA 1266

RESULT 13
ADI41706
ID ADI41706 standard; DNA; 1281 BP.
XX
AC ADI41706;
XX
DT 22-APR-2004 (first entry)
XX
DE Plant transcription factor polynucleotide #85.
XX
KW transgenic; plant; enhanced tolerance to abiotic stress;
KW glyphosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation;
KW branching pattern; apical dominance; trichome; cell proliferation;
KW root growth; root hair; seed development; plant size;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW plant anthocyanin; light response; shade avoidance; bioinformatic;
KW transcription factor; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN US2004019927-A1.
XX
PD 29-JAN-2004.
XX
PF 25-FEB-2003; 2003US-00374780.
XX
PR 18-APR-2001; 2001US-00837944.
XX
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
XX
PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PB;
PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX
DR WPI; 2004-132245/13.
DR P-PSDB; ADI41707.
XX
PT New transgenic plant comprising a recombinant polynucleotide of any one
PT of more than 500 nucleotide sequences, useful in bioinformatic search

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Db   601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGGCGGTAACGCCAAGCGACGTTGGGAAG  660

Qy   689 CTAAAACCGTTCGTTTGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT  748
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAAACCGTTCGTTTGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT  720

Qy   749 AACGTTTCCGTGAAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  808
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTGTTTGACTAAAGGTTGGAGCAGG  868
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG  840

Qy   869 TTCGTTAAGGAGAAGAGATCTACGTGCGTGGTGTTAGTTCAGTAGATCTAACGGT  928
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGAAGAGATCTACGTGCGTGGTGTTAGTTTCAGTAGATCTAACGGT  900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  988
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  960

Qy   989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCCGGAGAGTTCAAGAAAGACAGCGTCGTA  1048
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCCGGAGAGTTCAAGAAAACGACGTCGTA  1020

Qy  1049 GGAAACAAAGAGTGAACGATACTGAACGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC  1108
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAGAGTGAACGATACTGAACGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC  1080

Qy  1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTCTTTGTGTTTTAATAATT  1168
             ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db  1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTTTCTTTGTGTTTTAATAATT  1139

Qy  1169 TTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGGTTTCTTCTTCTTGTTTTACCAA  1228
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGGTTTCTTCTTCTTCTTGTTTTACCAA  1199

Qy  1229 AGGTTCATGAGTTGTTTTTGTGTATTGATGAACTGTAAAATTTATTTATAGGATAAATT  1288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTTGTGTATTGATGAACTGTAAAATTTATTTATAGGATAAATT  1259

Qy  1289 TTAAAAA  1295
             ||||||
Db  1260 TTAAAAA  1266
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RESULT 14
AD002166
ID   AD002166 standard; cDNA; 1281 BP.
XX
AC   AD002166;
XX
DT   01-JUL-2004 (first entry)
XX
DE   Thalecress transcription factor cDNA #290.
XX
KW   Thalecress; transcription factor; ss; gene; plant; transgenic;
KW   abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;
KW   phosphate limitation; potassium limitation; nitrogen limitation;
KW   hormone sensitivity; disease resistance; sugar sensing; seed germination;
KW   flowering; inflorescence architectural change;
KW   meristem cell differentiation; phyllotaxy; apical dominance;
KW   trichome development; seed development; premature senescence;
KW   delayed senescence; lethality; necrosis; plant size; leaf morphology;
KW   seed morphology; secondary metabolism; light response; shade avoidance.
XX
OS   Arabidopsis thaliana.
XX
PN   US2004045049-A1.
XX
PD   04-MAR-2004.
XX

PF   10-APR-2003; 2003US-00412699.
XX
PR   13-SEP-1999;   99US-00394519.
PR   21-JAN-2000; 2000US-00489976.
PR   17-FEB-2000; 2000US-00506720.
PR   22-MAR-2000; 2000US-00532591.
PR   22-MAR-2000; 2000US-00533029.
PR   22-MAR-2000; 2000US-00533030.
PR   22-MAR-2000; 2000US-00533392.
PR   22-MAR-2000; 2000US-00533648.
PR   06-APR-2000; 2000WO-US009448.
PR   16-NOV-2000; 2000US-00713994.
PR   27-MAR-2001; 2001US-00819142.
PR   17-APR-2001; 2001US-00837444.
PR   30-JAN-2002; 2002US-00958131.
PR   14-JUN-2002; 2002US-00171468.
PR   09-AUG-2002; 2002US-00225066.
PR   09-AUG-2002; 2002US-00225067.
PR   09-AUG-2002; 2002US-00225068.
PR   17-DEC-2002; 2002US-0434166P.
PR   25-FEB-2003; 2003US-00374780.
XX
PA   (ZHAN/) ZHANG J.
PA   (FROM/) FROMM M E.
PA   (HEAR/) HEARD J E.
PA   (RIEC/) RIECHMANN J L.
PA   (ADAM/) ADAM L J.
PA   (BROU/) BROUN P E.
PA   (PINE/) PINEDA O.
PA   (REUB/) REUBER T L.
PA   (KEDD/) KEDDIE J S.
PA   (YUGG/) YU G.
PA   (JIAN/) JIANG C.
PA   (SAMA/) SAMAHA R S.
PA   (PILG/) PILGRIM M L.
PA   (CREE/) CREELMAN R A.
PA   (DUBE/) DUBELL A N.
PA   (RATC/) RATCLIFFE O.
PA   (KUMI/) KUMIMOTO R.
PA   (SHER/) SHERMAN B K.
XX
PI   Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;
PI   Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
PI   Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
PI   Sherman BK;
XX
DR   WPI; 2004-225755/21.
DR   P-PSDB; AD002167.
XX
PT   New transgenic plant, useful in developing phenotypes with altered or
PT   improved characteristics or traits.
XX
PS   Claim 1; SEQ ID NO 579; 213pp; English.
XX
CC   The invention relates to a transgenic plant comprises a recombinant
CC   polynucleotide having a polynucleotide sequence or its complementary
CC   sequence comprising a sequence encoding a polypeptide, that initiates
CC   transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
CC   Rice, Rape or Corn, comprising any of the sequences appearing as AD001588
CC   -AD03527 or AD003530-AD03559. Also included are using a transgenic
CC   plant to grow a progeny plant, an expression cassette (comprising a
CC   constitutive, inducible or tissue-specific promoter and a recombinant
CC   polynucleotide described above), a host cell comprising the expression
CC   cassette, producing a modified plant having a modified trait, identifying
CC   a factor that is modulated by or interacts with a polypeptide encoded by
CC   the polynucleotide sequence and identifying at least one downstream
CC   polynucleotide sequence that is subject to a regulatory effect of any of
CC   the polypeptides encoded by the polynucleotide described above. The
CC   transgenic plant is useful for producing a plant that has an altered
CC   trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
CC   to chilling, germination in cold conditions,freezing tolerance, tolerance
CC   to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
CC   salt, tolerance to phosphate limitation, tolerance to potassium

CC   limitation, decreased sensitivity to nitrogen limitation), altered
CC   hormone sensitivity, reduced sensitivity to abscisic acid, an altered
CC   response to ethylene, disease resistance, altered susceptibility to
CC   Botrytis, altered susceptibility to Fusarium, altered susceptibility to
CC   Erysiphe, altered susceptibility to Pseudomonas syringae, altered
CC   susceptibility to Sclerotinia, altered sugar sensing, improved seed
CC   germination and seedling vigor, early flowering, late flowering, extended
CC   period of flowering, an inflorescence architectural change, a change in
CC   stem bifurcations, a lack of a shoot meristem, reduced meristem cell
CC   differentiation, altered phyllotaxy, altered branching pattern, reduced
CC   apical dominance, reduced trichome density, ectopic trichome development,
CC   altered trichome development, altered stem morphology, increased root
CC   growth, increased root hairs, altered seed development, altered cell
CC   proliferation/cell differentiation, premature senescence, delayed
CC   senescence, lethality, increased necrosis, an increase in seedling or
CC   plant size, a change in leaf morphology, increased
CC   altered leaf development, increased leaf size and mass, glossy leaves,
CC   leaf cell expansion, change in seed morphology, altered seed coloration,
CC   increased seed size, decreased seed size, altered seed shape, change in
CC   leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
CC   content, increased leaf insoluble sugars, decreased leaf insoluble
CC   sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
CC   content, an alteration of leaf glucosinolate content, change in seed
CC   biochemistry, an increase in seed oil content, decrease in seed oil
CC   content, increase in seed fatty acid content, decrease in seed fatty acid
CC   content, increase in seed protein content, decrease in seed protein
CC   content, alteration in seed prenyl lipid content, increase in seed
CC   sterols, upregulation of genes involved in secondary metabolism, increase
CC   in root anthocyanins, increase in plant anthocyanins, and alteration in
CC   light response or shade avoidance. The present sequence encodes a
CC   thalecress transcription factor of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match   95.9%; Score 1255; DB 12; Length 1281;
Best Local Similarity   99.9%; Pred. No. 4e-288;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

Qy   29 CACACACAAACACATTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGAT 88
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Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 148
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Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 120

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Db   181 TCAAGCGTTGTGTTAGATTCAGAGAAACGGCCTAGAAGCTGAATCTAGGAGGAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAG 328
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Db   301 AAACACCAGCCGCGTGGGCTCGGACATTCAACGAAGAAGACGAAGCCGCCGTCGTGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG 448
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Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGACGTCGATTTCTGAATTCTCATTCGAAATCTGAAATCTGAATCGTTGATATG 508
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Db   421 ATGGACGAAGACGAGACGTCGATTTCTGAATTCTCATTCGAAATCTGAAATCTGAATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGACAGAGATAAACGGCGTCGTAAATGGTAAC 568
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Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGACAGAGATAAACGGCGTCGTAAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTTCTACGACG 628
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Db   601 GGGTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTACCGTCAAGT 748
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Qy   749 AACGTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGCGTTAACGGGAAAGTGTGGAG 808
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Db   721 AACGTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGCGTTAACGGGAAAGTGTGGAG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
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Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGGAAGAATCTACGTGCTGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
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Db   841 TTCGTTAAGGAGGAAGAATCTACGTGCTGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

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Qy   989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGAGAAACGACGTCGTA 1048
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Db   1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTGTGGTGTAGCAAGAAGCAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTTTTCTTTGTGTTTAATAATT 1168
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Qy   1169 TTTAAAAACTCCATTTCGTTTTCTTTATTGCATCGGTTTCTTCTTCTTCTTGTTTACCAA 1228
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Qy   1229 AGGTTCATGAGTTGTTTTTGTTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT 1288
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Db   1200 AGGTTCATGAGTTGTTTTTGTTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
           |||||||
Db   1260 TTAAAAA 1266

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FT        /tag= a
FT        /product= "Arabidopsis thaliana transcriptional factor
          protein"
XX
PN   US2004098764-A1.
XX
PD   20-MAY-2004.
XX
PF   14-OCT-2003; 2003US-00685922.
XX
PR   16-MAR-2001; 2001US-00810836.
XX
PA   (HEAR/) HEARD J E.
PA   (RIEC/) RIECHMANN J L.
PA   (CREE/) CREELMAN R A.
PA   (RATC/) RATCLIFFE O.
PA   (KUMI/) KUMIMOTO R W.
PA   (GUTT/) GUTTERSON N.
PA   (REUB/) REUBER T L.
PA   (PINE/) PINEDA O.
PA   (LIBB/) LIBBY J M.
PA   (SHER/) SHERMAN B K.
XX
PI   Heard JE, Riechmann JL, Creelman RA, Ratcliffe O, Kumimoto RW,
PI   Gutterson N, Reuber TL, Pineda O, Libby JM, Sherman BK;
XX
DR   WPI; 2004-439639/41.
DR   P-PSDB; ADP67769.
XX
PT   New recombinant or isolated polynucleotide, useful for producing a
PT   transgenic plant having increased tolerance to abiotic stress (e.g., heat
PT   tolerance, chilling tolerance, germination in heat, and germination in
PT   cold).
XX
PS   Claim 1; SEQ ID NO 1; 117pp; English.
XX
CC   The present invention relates to plant transcriptional factor (TF)
CC   polypeptides and their encoding polynucleotides. The invention is useful
CC   for producing a transgenic plant having increased tolerance to abiotic
CC   stress, for increasing a plant's tolerance to abiotic stress, for
CC   producing commercially valuable plants and crops, for recombinant
CC   production (i.e. expression) of proteins, as regulators of plant gene
CC   expression, as diagnostic probes and for identifying exogenous or
CC   endogenous modulators of the transcription factors. The invention is also
CC   useful for screening libraries of molecules or compounds for specific
CC   binding and for creating transgenic plants having increased osmotic
CC   stress tolerance. The present sequence is a plant transcriptional factor
CC   cDNA.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;
```

Query Match   95.9%;   Score 1255;   DB 12;   Length 1281;
Best Local Similarity 99.9%;   Pred. No. 4e-288;
Matches 1266;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;

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Qy       29 CACACACCAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 88
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Db        1 CACACACCAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 60

Qy       89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCGTGTGAAACC 148
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Qy      149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACGGCCTAGAACGTGAATCTAGGAAGCTTCCGTCG 208
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Qy      209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCTGAAGAAGCTGAATCTGAGAAGCTTCCGTCG 268
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Qy      269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAGATGGGAGCTCAGATTTACCAG 328
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Qy      329 AAACACCAGCGCGTGTGCGCTCGGGACATTCAACGAAGGAGAAGAAGACCGCTCGTGCCTAC 388
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Db      301 AAACACCAGCGCGTGTGCGCTCGGGACATTCAACGAAGGAGAAGAAGACGCTCGTGCCTAC 360

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Db      421 ATGGACGAAGACGACAGGTCGATTCGTCGATTCTCCATTCGAAATCTGAAATCTCAGAAATCGTTGATATG 480

Qy      509 TTGAGGAAACATACTACTTATAACGAAGAGTTAGACGAGTAAACGGCGTCGTAATGGTAAC 568
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Db      481 TTGAGGAAACATACTATAACGAAGAGTTAGACGAGTAAACGGCGTCGTAATGGTAAC 540

Qy      569 GGAAACATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGACGGTGTTTCACGACG 628
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Db      541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGACGGTGTTTCTACGACG 600

Qy      629 GGGTTTAGATCGGCGAGGCACTGTTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
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Db      601 GGGTTTAGATCGGCGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy      689 CTAAACCGTTGGTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 748
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Db      661 CTAAACCGTTGGTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy      749 AACGTTTCCGTGAAAGGAGTGTGTTGTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
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Qy      809 TTTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG 868
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Db      781 TTTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG 840

Qy      869 TTCGTTAAGGAGAAGAATCTACGTGGTGGTCGTGGTTAGTTCAGTAGATCTAACGGT 928
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Qy      989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAAACGACGTCGTA 1048
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Qy     1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTCTTCTTC-TTTTTTTTTTTTTGTTTAATAATT 1168
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Qy     1289 TTAAAAA 1295
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Post-processing: Minimum Match 0%
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SUMMARIES

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2	389.8	29.8	1239	4	US-09-810-836B-1	Sequence 1, Appli
3	170.2	13.0	563	4	US-09-640-211A-230	Sequence 230, App
4	142.2	10.9	365	4	US-09-640-211A-1189	Sequence 1189, Ap
5	118.6	9.1	378	4	US-09-640-211A-1421	Sequence 1421, Ap
6	112.2	8.6	521	4	US-09-640-211A-238	Sequence 238, App
7	112.2	8.6	521	4	US-09-640-211A-1210	Sequence 1210, Ap
c 8	58.2	4.4	612	4	US-09-902-540-1357	Sequence 1357, Ap
c 9	57.2	4.4	240	1	US-08-628-417-6	Sequence 6, Appli
c 10	55.8	4.3	751	4	US-09-533-029-81	Sequence 81, Appl
c 11	55.4	4.2	7218	1	US-08-232-463-14	Sequence 14, Appl
c 12	55	4.2	362	4	US-09-621-976-16010	Sequence 16010, A
c 13	55	4.2	1696	1	US-09-835-811-1	Sequence 1, Appli
c 14	54.4	4.2	365	4	US-09-621-976-16042	Sequence 16042, A
c 15	54.4	4.1	371	4	US-09-621-976-16048	Sequence 16048, A
c 16	53.6	4.1	359	4	US-09-621-976-16019	Sequence 16019, A
c 17	53.6	4.1	2447	2	US-09-014-969-14	Sequence 14, Appl
c 18	53.6	4.1	3275	3	US-09-370-838-151	Sequence 151, App
c 19	53.6	4.1	3275	4	US-09-854-133-151	Sequence 151, App
c 20	53.4	4.1	396	4	US-09-640-173-53	Sequence 53, Appl
c 21	53.4	4.1	396	4	US-09-713-550-53	Sequence 53, Appl
c 22	53.4	4.1	396	4	US-09-825-294-53	Sequence 53, Appl
c 23	53.4	4.1	396	4	US-09-970-966-53	Sequence 53, Appl
c 24	53.2	4.1	359	4	US-09-621-976-16008	Sequence 16008, A
c 25	52.8	4.0	2262	4	US-09-311-021-171	Sequence 171, App
c 26	52.6	4.0	357	4	US-09-621-976-16058	Sequence 16058, A
c 27	52.2	4.0	441	4	US-09-601-537-10	Sequence 10, Appl
c 28	52.2	4.0	4121	4	US-09-601-537-9	Sequence 9, Appli
c 29	51.4	3.9	578	3	US-09-602-877A-95	Sequence 95, Appl
c 30	51.4	3.9	1117	3	US-09-247-373B-33	Sequence 33, Appl
c 31	51.4	3.9	1798	3	US-09-797-906-1	Sequence 1, Appli
c 32	51.2	3.9	1039	1	US-09-902-540-1280	Sequence 1280, Ap
c 33	51	3.9	144	4	US-08-702-344-26	Sequence 26, Appl
c 34	50.6	3.9	1459	4	US-09-537-654-3	Sequence 3, Appli
c 35	50.6	3.9	6671	1	US-08-280-443-1	Sequence 1, Appli
c 36	50.6	3.9	6671	1	US-08-457-459-1	Sequence 1, Appli
c 37	50.6	3.9	6671	1	US-08-555-678-1	Sequence 1, Appli
c 38	50.6	3.8	6671	5	PCT-US95-02275-1	Sequence 1318, Ap
c 39	50	3.8	614	4	US-09-902-540-1318	Sequence 33, Appl
c 40	49.8	3.8	2394	4	US-09-800-729-33	Sequence 3, Appli
c 41	49.4	3.8	2146	4	US-10-003-392-3	Sequence 1, Appli
c 42	49.4	3.8	6243	2	US-10-056-075-1	Sequence 10, Appl
c 43	49	3.7	1051	3	US-09-245-041-10	Sequence 10, Appl
c 44	49	3.7	1051	4	US-09-358-055B-10	Sequence 10, Appl
c 45	49	3.7	1051	4	US-09-893-238-10	

ALIGNMENTS

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RESULT 1
US-09-533-029-65
; Sequence 65, Application US/09533029
; Patent No. 664446
; GENERAL INFORMATION:
;  APPLICANT: Heard, Jacqueline
;  APPLICANT: Broun, Pierre
;  APPLICANT: Riechmann, Jose-Luis
;  APPLICANT: Keddie, James
;  APPLICANT: Pineda, Omaira
;  APPLICANT: Adam, Luc
;  APPLICANT: Samaha, Raymond
;  APPLICANT: Zhang, James
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT: Ratcliffe, Oliver
;  APPLICANT: Pilgrim, Marsha
;  APPLICANT: Jiang, Cai-Zhong
;  APPLICANT: Reuber, Lynne
;  TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
;  FILE REFERENCE: MBI-010
;  CURRENT APPLICATION NUMBER: US/09/533,029
;  CURRENT FILING DATE: 2000-03-22
;  EARLIER APPLICATION NUMBER: 60/125,814
;  EARLIER FILING DATE: 1999-03-23
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 65
;  LENGTH: 1281
;  TYPE: DNA
;  ORGANISM: Arabidopsis thaliana
;  FEATURE:
;  OTHER INFORMATION: G867
US-09-533-029-65

Query Match             95.9%;  Score 1255;  DB 4;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1266;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGAT 88
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGAT 60

Qy         89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGGTTCCATCTGTGAAACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGGTTCCATCTGTGAAACC 120

Qy        149 CCGGCGATAACTCCGGCGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCCGGA 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGCGATAACTCCGGCGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCCGGA 180
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Db     1260 TTAAAAA 1266
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RESULT 2
US-09-810-836B-1
; Sequence 1, Application US/09810836B
; Patent No. 6835540
; GENERAL INFORMATION:
;   APPLICANT: Broun, Pierre
;   TITLE OF INVENTION: METHOD FOR MODIFYING A BIOSYNTHETIC
;   TITLE OF INVENTION: PATHWAY
;   FILE REFERENCE: 51442001200/MBI0032
;   CURRENT APPLICATION NUMBER: US/09/810,836B
;   CURRENT FILING DATE: 2001-03-16
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: PatentIn Version 4.0
SEQ ID NO 1
;   LENGTH: 1239
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (6)...(1091)
;   OTHER INFORMATION: G993
US-09-810-836B-1

  Query Match             29.8%;  Score 389.8;  DB 4;  Length 1239;
  Best Local Similarity   64.5%;  Pred. No. 8.9e-100;
  Matches  668;  Conservative   0;  Mismatches 322;  Indels 45;  Gaps  4;
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Qy   159 CTCCGGCGAAAAGTCGTCGGTAGTAACTATACAGGATGGGAAGCCGATCAAGCGTTG 218
             | |||| |||||| | || ||| ||  |  | | || || | |||  | | |||
Db   103 CTTCTCCGCCGGCGACGTCGATCGATCGGTCTCTACAGAATGGGAAGCGGCGAAGCAGCGTCG 162

Qy   219 TGTTTAGATTCAGAGAACCGGCGTAGAAGCTTGAATCTAGAGAAGCTTCCGTCGTCAAAATACA 278
             || | ||||||||||||| |||| || || || || |||||||||  || || ||
Db   163 TTTTGGATTCAGAGAACCGGCGTCCAGACCGAGTCACGTAAGCTTCCTTCGTCGAAATATA 222

Qy   279 AAGGTGTGTGCCACACCAACCAAACGGAGATGGGAGCTCAGATTTACGAGAAACACCAGC 338
             |||| | |||| |  ||| ||| |||||||||||| |||||||||||| || || ||
Db   223 AAGGCGTTGTGCCTCAGCCTAACGGAGAATGGGAGCTCAGATTTACGAGAAGCATCAGC 282

Qy   339 GGGTGTGGCTCGGGACATTCAACGAGAAGACGAAGCCGCTCGTCGCCTACGACGTCGCGCG 398
             || || |||||| | |||||||| || ||| || |||||| ||| | ||| || |||||
Db   283 GAGTTGGCTCCGGTACTTTCAACGAGGAGAAGAAGCCGCTCGTCGTCGTCTTACGACATCGCCG 342

Qy   399 TTCACAGGTTCCGTCGCCGTAGTAACTATCAGCCGTCACAAATTCAAA---GACGTGAAGATGGACG 455
             || |||| |||||| ||   ||| || || || | ||| | || ||||
Db   343 TGAGGAGATTCCGGCGTTTCCGGCGCCCGTCACTAACTTCAAATCTCAAGTTGATGGAAACG 402

Qy   456 AAGACGAGGTCGATTCTCATTCGAAATCTGAGATCGTTGTGATATGTTGAGGA 515
             | |||  | | |||||||| |  || ||||| | ||||||| || |||||||
Db   403 ACGCCGAATCGGCGTCTTTCTTGACGCTCATTCTAAAGCTGAGATCGTGGATATGTTGAGGA 462

Qy   516 AACATACTTATAACGAAGAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGAAACA 575
             ||||  |||| || |||    || |||
Db   463 AACACACTTACGCCGATGAGTTTGAGCAGAGTAGACGGAAGTTTGTTAACGGCGACGGGAA 522

Qy   576 TGACTAGGACGTTGTTAACGTCGGGGTGTAGTAATGATGTGTTCTACGACGCGGGTTTA 635
             |||||| ||| |||||||||| || ||| || ||  |||  ||||| |||||||
Db   523 AACGCTCYGGGTTGGAGACGGCCAAGCGGTACGGACGCGGAAACGACCTGTGTT---------TTGA 570

Qy   636 GATCGGCGGAGGCACTCGTTGTGAGAAAGGGCGTAACCGCGGAAGCTAAACC 695
             | ||  || ||| |||| || |||   | ||  |||||
Db   571 GAGCGCGTGAGGTTTGTTCGAAAGACGTGTTACGGCGACGTCGGGAAGCTGAACC 630

Qy   696 GTTTGGTTATACCGAAACATCACCGAGAAACATTTTCCGTCAAGTAACGTTT 755
             |||||  || ||   ||| ||  ||  | || | |||| |||||| ||
Db   631 GTTTAGTGATACCGGAACAACAACACGCGGAAGCATTTTCCGTTACCGGCGATGACGACGACG 690

Qy   756 CCGT----------------------------------GAAAGGAGTGTTGTTAACTTTGACGTTAACG 794
             | |||
Db   755
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Qy   209 TCAAGCGGTTGTGTTAGATTCAGAGAACCGGCTGAAAGCGTGAATCTAGAGAAGCTTCCGTCG 268
             |||||||||||||||| |||||||||||||||| ||||||||||||||||||||| |||||
Db   181 TCAAGCGGTTGTGTTAGATTCAGAGAACCGGCGTGAATCTAGAGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAGAGATGGGAGCTCAGATTTACGAG 328
             ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAGAGATGGGAGCTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCCGGTGTGCTCGGGCTCGGGACAGAACGAAGAGAAGACGAAGCCGCTCGTCGCCTAC 388
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCGCCGGTGTGCTCGGGCTCGGGACAGAACGAAGAGAAGACGAAGCCGCTCGTCGCCTAC 360

Qy   389 GACGTCGGGTTCACAGGTTCCGTCGACGACGCGTCCGTGCCGTCACAAATTTCAAAGACGTGAAG 448
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGGTCGATTCTCATTCGAAATCTGAGATCGTTGATATG 508
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAAGACGAGGTCGATTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGACGAGTAAACGGCGTCGTAATGGTAAC 568
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGACGAGTAAACGGCGTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGACGTAATGATGGTTTCTACGACG 628
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGACGTAATGATGGTTTCTACGACG 600

Qy   629 GGGTTTAGATCGGCGGAGGCACTCGTTGAGAAAGCGGTAACGGCCAAGCGGTTGGGAAG 688
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTTAGATCGGCGGAGGCACTCGTTGAGAAAGCGGTAACGGCCAAGCGGTTGGGAAG 660

Qy   689 CTAAACCGTTTGTTATACCGAAACATCACGCCGAAACATCACGAGAAACATTTTCCGTCAAGT 748
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGGTTATACCGAAACATCACGAGAAACATTTTCCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGAGTGTGTTGAACTTTGAGACGTTAACGGGAAAGTGTGGAGG 808
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGAGAGTGTTGAACTTTGAGACGTTAACGGGAAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGAGAATCTACGGTCGTGTGGTTGGTTAGTTTCAGTAGATCTAACGGT 928
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGAGAATCTACGGTCGTGTGGTTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTCGGAAGTCGAGATCTCGGGTCAGATTTAGATGCGGGT 988
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTCGGAAGTCGAGATCTCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTTGAGATTGTTCCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy  1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1108
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTTCACGCCTCGTAACAACTCTTCTTC----TTTTTTTCTTTCTTTTGTTTAATAATT 1168
             ||||||||||||||||||||||||||||       |||||  |||||| ||| ||||||||
Db  1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTCTTTTGCATCGGTTTATAATATT 1139

Qy  1169 TTTAAAAACTTCCATTTCGTTTCTTATTTGCATCGGTTTCTTGTTTACCAA 1228
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAAACTTCCATTTTCGTTTCTTATTTGCATCGGTTTCTTGTTTACCAA 1199

Qy  1229 AGGTTCATGAGTTGTTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259
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Db   691  CGATGGGATGAATCCGTTCCGACGAAAGGCGTTTGATTAACTTGGAAGATAGAACAG  750
               ||||||  ||| ||||||| ||||| ||||  |||||||||||  |||||||||||
Qy   795  GGAAAGTGTGGAGGTTCGGTTCCGTTACTCGTTATTGGAACAGTAGTCAGAGTTGTTTGACTA  854
               ||||||||||||||||||| |||||||||| |||||||
Db   751  GGAAAGTGTGGCGGTTCCGTTACGTACTGGAACAGCAGTCAAAGTTACGTGTTGACCA  810
               |||||||||||||||||||| |||  ||||||  |||
Qy   855  AAGGTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTGTGTGGTTAGTTTCA  914
               ||||||||||||||||||  |||||||||||||||  ||||||||
Db   811  AGGGCTGGAGCCCGTTCGTTAAAGAGAAGAATCTTCGAGCCGTGATGTGGTTTGTTTCG  870
               |||||||||||||||  ||||||||||||||||||||  |||
Qy   915  GTAGATCTAACGTCAGGATCAACAGTTGTACATTGGGTGGGAAGTCGAGATCCGGGTCAG  974
               ||| ||| |||||||||  |||  ||||  || ||  ||||||||||||||
Db   871  AGAGATCAACCGGACCAGACCGGCAATTGTATATCCACTGGAAAGTCCGGTTCAGTCCGG  930
               ||||| ||||||||||||||||||||||||||||||||||||
Qy   975  ATTTAGATGCGGGTTCGGGGTTTGAGATTGTTCGGAGTTAACATTTCAATGTGAGTAACGAGAAACCAA  1034
                   |||||||||||||||||||||||||  |||||||||||||||||
Db   931  TTCAGACTGTGGTTAGGCTATTCGGAGTCAACATTTTCAATGTGAGTAACGAGAAATGTTATCGT  990
               |||||||||||||||||||||||||||  ||||||||||||||
Qy  1035  GAAACGACGTCGTA--------GGAAACAAAAGAGTGAAGACGATACTGAGATGTTATCGT  1085
                    |||||||||  |  |||  |||
Db   991  ACGACGTCGCAGTAGAGTGTGTTGGCAAGAAGACATCTCGGGAAGATGATTGTTTTCGT  1050
               ||||||||||||||||||||||||||||||||||||
Qy  1086  TGGTGTGTAGCAAGAAGCAACGCATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTT  1145
               ||||||||||||||||||  |||
Db  1051  TAGGGTGTTCCAAGAAGCAGCAGGCGATTATCAACATCTTGGACAAATTCTTTTTTTTGT  1110
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Qy  1146  TTTCTTTTGTTGTTT  1160
               ||||||  ||||||
Db  1111  TTTTTTTCTTCAATTT  1125
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RESULT 3
US-09-640-211A-230
; Sequence 230, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
;   APPLICANT: Wood, Marion
;   APPLICANT: Shenk, Michael A.
;   APPLICANT: McGrath, Annette
;   APPLICANT: Glenn, Matthew
;   TITLE OF INVENTION: Compositions and Methods for the
;   TITLE OF INVENTION: Modification of Gene Transcription
;   FILE REFERENCE: 11000.1021C1U
;   CURRENT APPLICATION NUMBER: US/09/640,211A
;   CURRENT FILING DATE: 2000-08-16
;   NUMBER OF SEQ ID NOS: 2368
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230
;   LENGTH: 563
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
US-09-640-211A-230

Query Match             13.0%;  Score 170.2;  DB 4;  Length 563;
Best Local Similarity   61.5%;  Pred. No. 7.1e-38;
Matches    312;  Conservative    0;  Mismatches  183;  Indels   12;  Gaps    2;

Qy   460  CGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAAATCGTTGATATGTTGAGGAAACA  519
              | ||||| |||||||  |||  ||| ||||  ||||||| ||  ||||| |||||
Db     2  CGAGGCCGACTTCCTGCCAAACACTCCAGACCCGAGATCGTCGCACATGCTCGCGCAAGCA  61
              |||  |||||||
Qy   520  TACTTATAACGAAGAGTTAGACAGCAGAGTAAACGCGTCGTAATGCGCCTCGTTAACGGCG  579
              |||||||||||| |||||  ||||  |||  ||| |||||||||
Db    62  CACGTACCGCGACGAGCTAGAGCAGGCAACAGCAAGGGCTTCCGCGCCGGCCAAGCA  121
              |||||  ||||||||  |||||  |||
Qy   580  TAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGGTTTAGATC  639
                   ||||||||||||| |||||||||||||||||  |||||
Db   122  GGCCGGAGGGGGCACTGTTTGAGAAGGCGTAACGCCCAAGCGACGTTGGGAAGGCTAACCGTTT  699
              |||||||||||||||  |||||||
Qy   640  GGCGGAGGCACTGTTTGAGGGTTCGGCCGGTTCGGCGGGTCGGCCGCCCG-------C  172
                   ||||||||||||||||||||||
Db   173  CCGGGAGCAGCTGTTCCGAGAGGCCCGTGACGGCCGGCGACGTGGGGAAGCTGAACCGGCT  232
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RESULT 4
US-09-640-211A-1189
; Sequence 1189, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
;   APPLICANT: Wood, Marion
;   APPLICANT: Shenk, Michael A.
;   APPLICANT: McGrath, Annette
;   APPLICANT: Glenn, Matthew
;   TITLE OF INVENTION: Compositions and Methods for the
;   TITLE OF INVENTION: Modification of Gene Transcription
;   FILE REFERENCE: 11000.1021C1U
;   CURRENT APPLICATION NUMBER: US/09/640,211A
;   CURRENT FILING DATE: 2000-08-16
;   NUMBER OF SEQ ID NOS: 2368
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1189
;   LENGTH: 365
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(365)
;   OTHER INFORMATION: n = A,T,C or G
US-09-640-211A-1189

Query Match             10.9%;  Score 142.2;  DB 4;  Length 365;
Best Local Similarity   69.1%;  Pred. No. 4.5e-30;
Matches    208;  Conservative    0;  Mismatches   90;  Indels    3;  Gaps    1;

Qy   666  TAACGGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGGAAACATCACGCAGAGA  725
              | ||||||||||||||||||||||||||||||||
Db     1  TGACGGCCGAGCGACGTGGGGAAGCTCAAGCGTGATCCCGAAGCAGCAGCGGAGA  60
              |||||||||||||||||||
Qy   726  AACATTTCCGTTACCGTCAAG---TAACGTTCCGCCGGCCGGCCGGCCGGCCGGCGG  782
                  ||||||||||||||||||   |||||||||
Db    61  AGCACTTCCCCGTGCCGGCCGCCCGCGATGAAGGGCGTACTGCTCAACTTCG  120
              ||||||||||||||  |||||  |||||
Qy   783  AGGACGTTAACGGAGAAGTGTGGAGGTTCCGTTACTCGTTATTGGAACAGTAGTCAGAGTT  842
                  ||||||||||||||||||||||
Db   121  AGGACGTCGGCGGGAAGGGTGTGGCGGTTCCGTTATTCGTTACTGGAACAGCAGCCAGAGCT  180
              ||||||||||||||  |||
Qy   843  ATGTTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGGAGAAGAATCAACAGTTGTACATGAC  902
                   ||||||||||||||||||||||||
Db   181  ACGTGCTCACCAAGGTTGAGCCGGTTCGTTGCGGAGGAGAAGAGCCTGGAAGGCCGGCCGGCACA  240
              ||||||||||||||||||||
Qy   903  TGGTTAGTTTCAGTTAGTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGTGACG  962
                   ||||||||||||||||||||
Db   241  CCGTNTGCTTCCAGCGTCGCACCGGCCGGCGACGAGCAGCTNTACATCGACTTCAAGCCGC  300

Qy   963  G  963
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Db   301 G 301

RESULT 5
US-09-640-211A-1421
; Sequence 1421, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1421
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(378)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-211A-1421

Query Match   9.1%; Score 118.6; DB 4; Length 378;
Best Local Similarity   60.6%; Pred. No. 2.2e-23;
Matches 234; Conservative   0; Mismatches 140; Indels 12; Gaps   2;

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Qy  460 CGAGGTGATTTCTGATTTCTCATTCGAAATCTGAATTCGTTGATATGTTGAGGAAACA 519
        |||||  ||  ||  || || ||||  ||||  || ||| ||| ||||||||||
Db    2 CGAGGCCGACTTCCTGGCCAAACACTCCAAGCCCGAGATCGTCGACATGCTGCGCAAGCA 61

Qy  520 TACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGAAACATGAC 579
        |||  |  ||| |||||||| ||| |||||||| ||  |  || ||  ||  ||||||
Db   62 CACGTACCGCGACGAGCAGAGCAGAGCAGCGGCGCTACACAGGGGTCCGCGCCGGAACG 121

Qy  580 TAGGACGTTGTTAACGTCGGGGTGAGTAATGATGGTGTTTCTACGACGGGGTTAGATC 639
        ||||  |||  ||||  ||  |||| |||||| |  ||  |
Db  122 GGCCGGAGGGGGGCGGTTCGGGCGGGACAGAGTGGTCCGCCGCCG--------C 172

Qy  640 GGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTT 699
        |||| ||||||| ||||||||||| |||||| ||| |||| |||||||| ||||||
Db  173 CCGGGAGCAGCTGTTCGAGAAGGCCGTGACGCCGAGAAGCAGCACTTCCCCGCT 232

Qy  700 GGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTAACGTCAAG---TAACGTTTC 756
        |||| |||||| |||||||| || ||  |  |||||  |||
Db  233 GGTGATCCCGAAGCAACACGCGAGAAGCGCCGAGAGTCGGGGAAGTGTGGCGCGGCGGAC 292

Qy  757 CGTGAAACGAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCGTTA 816
        ||||||| ||||| || |||| ||| | |
Db  293 GATGAAGGGCGTACTGCTCAACTTCGAGGAGCGTGCGGCGGGAAGTGTGGGCGGGTTCCGGTA 352

Qy  817 CTCGTATTGGAACAGTAGTCAGAGTT 842
        ||| |||||||||| |
Db  353 TTCGTACTGGAACAGCAGCCAGAGCT 378
```

RESULT 6
US-09-640-211A-238
; Sequence 238, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-238

Query Match   8.6%; Score 112.2; DB 4; Length 521;
Best Local Similarity   66.8%; Pred. No. 1.7e-21;
Matches 181; Conservative   0; Mismatches 78; Indels 12; Gaps   1;

```
Qy  644 GAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTT 703
        ||||| ||||| |||||  |  ||||| ||| |||||| ||| ||||| |||  |  ||
Db  246 GAGCCCATGTTCGAGAAGCCGCTGACGCCGAGCGACGTGGGGAAGCTGAACAGCGTGGTG 305

Qy  704 ATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTCCGTGAAA 763
        ||||||||  |  || |||| |||  ||  ||||||||
Db  306 ATACCGAAGCAGCAGCGCGGAGAAGCAGCACTTCCCGCT----------GGTGGGCGAGGGCG 353

Qy  764 GGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCGTTACTTCGTAT 823
        |||||||| |  |||| |||||  |  |  ||||||||| ||||||||| ||||| ||
Db  354 ACCCAGCAGCTGAGCTTCGAGGACGAGCGAGTCCGGGAAGTGTGGGAGGTTCCGCTACTCCTAC 413

Qy  824 TGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCGTTCGTTCCTTCGTTCTTCA 883
        ||||| |||||||| ||| ||| |||| ||||||| ||||||||| |||||||||
Db  414 TGGAGCAGCAGCCAGAGCTACGTTCCTCACCAAGGGCTGAGCCGTCGTTAGTTCA 473

Qy  884 AATCTACGTGCTCGTGACGTGGTTAGTTCA 914
        |  |||||||||||||
Db  474 CGCCTCGACGCCGGGACGTGGTCCTCCTCA 504
```

RESULT 7
US-09-640-211A-1210
; Sequence 1210, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1210
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1210

Query Match   8.6%; Score 112.2; DB 4; Length 521;
Best Local Similarity   66.8%; Pred. No. 1.7e-21;
Matches 181; Conservative   0; Mismatches 78; Indels 12; Gaps   1;

```
Qy  644 GAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTT 703
        ||||| ||||| |||||  |  ||||| ||| |||||| ||| ||||| |||  |  ||
Db  246 GAGCCCATGTTCGAGAAGCCGCTGACGCCGAGCGACGTGGGGAAGCTGAACAGCGTGGTG 305

Qy  704 ATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTCCGTGAAA 763
        ||||||||  |  || |||| |||  ||  ||||||||
Db  306 ATACCGAAGCAGCAGCGCGGAGAAGCAGCACTTCCCGCT----------GGTGGGCGAGGGCG 353

Qy  764 GGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCGTTACTTCGTAT 823
        |||||||| |  |||| |||||  |  |  ||||||||| ||||||||| ||||| ||
Db  354 ACCCAGCAGCTGAGCTTCGAGGACGAGCGAGTCCGGGAAGTGTGGGAGGTTCCGCTACTCCTAC 413
```

Qy   824 TGGAACAGTAGTCAGAGTATGTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGAGAAG 883
           ||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   414 TGGAGCAGCAGCCAGAGCTACGTCCTCACCAAGGGCTGGAGCGCGCTTCGTCAAGGACAAG 473

Qy   884 AATCTACGTGCTGGTGACGTGGTGGTAGTTTCA 914
           || ||| |||||||||| |||||||
Db   474 CGCCTCGACGCCGCGGGACGTGGTCCTCTTCA 504

RESULT 8
US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1357
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match   4.4%;   Score 58.2; DB 4; Length 612;
Best Local Similarity   60.0%;   Pred. No. 3.5e-06;
Matches   96; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   1131 TCTTCTCCTTTTTTTTTTTTTTCTTTTGTTGTTTAATAATTTTTAAAAACTCCATTTTCGTTT 1190
           |||||||||||||||||||| ||| |||| || ||||||||||| |||||
Db   330 TTTTTTTTTTTTTTTATTTAANTTTTTTTTTTTTTTTAATTTTTTTTTATTTTTTTA 271

Qy   1191 TCTTTATTTGCATCGGTTTCTTCTTCCTTGTTTACCAAAGGTTCATGAGTTGTTTTTGTT 1250
           ||||||||| ||| ||| ||||||||||||||||| || |||||
Db   270 TTTTTATTTTATTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTT 211

Qy   1251 GTATTGATGAACTGTAAATTTTATTTATAGGATAAATTT 1290
           ||| ||||| ||| |||| ||||||
Db   210 TTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTATTTTT 171

RESULT 9
US-08-628-417-6/c
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESSEE: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligodeoxynucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-628-417-6

Query Match   4.4%;   Score 57.2; DB 1; Length 240;
Best Local Similarity   58.0%;   Pred. No. 3.8e-06;
Matches 101; Conservative   0; Mismatches   73; Indels   0; Gaps   0;

Qy   1131 TCTTCTCCTTTTTTTTTTTTTTCTTTTGTTGTTTAATAATTTTTAAAAACTCCATTTTCGTTT 1190
           |||||||||||||||||||| |||||| ||||
Db   187 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 128

Qy   1191 TCTTTATTTGCATCGGTTTCTTCTTCCTTGTTTACCAAAGGTTCATGAGTTGTTTTTGTT 1250
           | |||||| ||| ||||||||||||||||||
Db   127 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 68

Qy   1251 GTATTGATGAACTGTAAATTTTATTTATAGGATAAATTTTAAAAAGGGTTACTT 1304
           || ||||| ||| |||| ||||||
Db   67 TTTTTTTTTTTTTTTTTTTTTTTAGTAAAATTATTTCTAAAGTTTTATT 14

RESULT 10
US-09-533-029-81
; Sequence 81, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 751
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G25

US-09-533-029-81

Query Match   4.3%; Score 55.8; DB 4; Length 751;
Best Local Similarity 59.6%; Pred. No. 1.9e-05;
Matches 115; Conservative   0; Mismatches 72; Indels   6; Gaps   1;

Qy   275 TACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGA------G 328
          |||||||| ||||| ||||||||||||||| ||||||| || |
Db   227 TACAGAGGGATAAGGCAGAGGCCATGGGGCAAATGGGCCAGCCGGAGATTCGTGACCCGAGC 286

Qy   329 AAACACCAGCCGCGTGTGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCTAC 388
          ||| |||||| |||||||||||||||||| ||||||| |||||| |||||
Db   287 AAAGGTGTACGTGTCTGGCTTGGCACATTCAAAACCGCGACGAAGCTGCTCGAGCCTAC 346

Qy   389 GACGTCGCGGTTCACAGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
          |||||||| |||||||||| ||||||||||| ||||||| |||||||||||| |||||
Db   347 GACGTTGCTGCCATCAAAATCCGTGCCGGAAAGCCAAACTGAATTTCCCAAACACTCAA 406

Qy   449 ATGGACGAAGACG 461
          |||||||||||||
Db   407 GTAGAAGAAGAAG 419

RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: , SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match   4.2%; Score 55.4; DB 1; Length 7218;

Best Local Similarity   4.7%; Pred. No. 9.3e-05;
Matches   17; Conservative 203; Mismatches 139; Indels   0; Gaps   0;

Qy   66 AAACCATAAAAAAAAACAGATTAAATGGAATGGAGTAGCGGTTGATGAGAGTACTACAA 125
          ::: :::::::::::::::: ::: ::: :::: :::: :: :::::
Db   1399 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1340

Qy   126 GTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCCGTAGTA 185
          : : ::: :: :::: : ::::::::::: ::::::: ::::::::::
Db   1339 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1280

Qy   186 ACTTATACAGGATGGGAAGCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCCTAGAAG 245
          :::: ::: ::::: :::::::::::::::: :::::::::::::::::::::::::::::
Db   1279 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1220

Qy   246 CTGAATCTAGGAGCTTCCGTCGTCAAAATACAAAGGTGTGTGCCACAACCAAACGGAA 305
          ::: :::::::::::: :: :::::::::: ::::: :: :::::::::::::::::::
Db   1219 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1160

Qy   306 GATGGGGAGCTCAGATTTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAG 365
          :::::::::: ::: :::::::::::::::::::::::::::::::::::::: ::::::
Db   1159 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1100

Qy   366 AAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCC 424
          :::::::::: ::: :::::::: ::: ::::::::::::::::: ::||||| |||||
Db   1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCCTCGACCTGCAGCC 1041

RESULT 12
US-09-621-976-16010/c
; Sequence 16010, Application US/0961976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16010
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16010

Query Match   4.2%; Score 55; DB 4; Length 362;
Best Local Similarity 58.4%; Pred. No. 2.1e-05;
Matches   94; Conservative   1; Mismatches 66; Indels   0; Gaps   0;

Qy   1130 CTCTTCTCTTTTTTTTTTCTTTGTTGTTTAATAATTTTAAAAACTCCATTTTCGTT 1189
          | |||| ||||||||||||| ||||| |||||||||||||||||| |||
Db   362 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 303

Qy   1190 TTCTTTATTTGCATCGGTTCTTCTTCTTGTTGTTACCAAAGGTTCATGAGTTGTTTTGT 1249
          | ||| ||||||||||||||||| ||||| ||||| |||||||||||| ||||||||||
Db   302 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATAGAATGAGGCTTGGTTTGTTGTTTTTA 243

Qy   1250 TGTATTGATGAACTGTAAATTTTATTTATTATAGGATAAATTTT 1290
          |||||||||||||||||||| |||| ||||||||| |||||
Db   242 AATTTTTTCTATTTCTATTATTTTCTATCGAATTATTTTT 202

RESULT 13
US-09-835-811-1/c
; Sequence 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL0012228
; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
US-09-835-811-1

Query Match   4.2%;   Score 55; DB 4; Length 1696;
Best Local Similarity   57.1%;   Pred. No. 5.1e-05;
Matches 100; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy   1131 TCTTCTCTCTTTTTTTTTTTCTTTGTTGTTTAATAATTTTAAAAAACTCCATTTTCGTTT 1190
          || || ||||||||||| |||| | ||||| || ||||
Db   1668 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1609

Qy   1191 TCTTTATTTGCATCGGTTTCTTCTCTGTTTACCAAAGGTTCATGAGTTGTTTTGTT 1250
          | ||||| ||| |||||||||||||||||||||||||||||||
Db   1608 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1549

Qy   1251 GTATTGATGAACTGTAAATTTATTATAGGATAAATTTAAAAAGGGTTACTTA 1305
          | ||- | |||| ||| ||-|-| |||||||||||
Db   1548 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAATCTATACAGTGATCCTTA 1494

RESULT 14
US-09-621-976-16042/c
; Sequence 16042, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16042
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16042

Query Match   4.2%;   Score 54.4; DB 4; Length 365;
Best Local Similarity   58.8%;   Pred. No. 3e-05;
Matches 94; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy   1131 TCTTCTCTCTTTTTTTTCTTTGTTGTTTAATAATTTTAATAATTTTAAAAAACTCCATTTTCGTTT 1190
          || || ||||||||||| |||| | ||||| |||
Db   361 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 302

Qy   1191 TCTTTATTTGCATCGGTTTCTTCTCTGTTTACCAAAGGTTCATGAGTTGTTTTTGTT 1250
          | ||||| ||| |||||||||||||||||||||||
Db   301 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATAGAATGAGGCTTGGTTTGTTTTTTAA 242

Qy   1251 GTATTGATGAACTGTAAATTTATTTATTATAGGATAAATTT 1290
          | ||- | |||| ||| |||||||||||
Db   241 ATTTTTTCTATTTCTATTATTTTCTATCGAATTATTTTT 202

RESULT 15
US-09-621-976-16048/c
; Sequence 16048, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16048
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16048

Query Match   4.2%;   Score 54.4; DB 4; Length 371;
Best Local Similarity   58.8%;   Pred. No. 3.1e-05;
Matches 94; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy   1131 TCTTCTCTCTTTTTTTTTCTTTGTTGTTTAATAATTTTAATAATTTTAAAAAACTCCATTTTCGTTT 1190
          || || ||||||||||| |||| | ||||| || |||||
Db   362 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTKKTTTTTTTTTTTTTT 303

Qy   1191 TCTTTATTTGCATCGGTTTCTTCTCTGTTTACCAAAGGTTCATGAGTGTTTTTTGTT 1250
          | ||||| ||| |||||||||||||||||||||||
Db   302 TTTTTTTTTTTTTTTTTTTTTTTTTTTTCATAGAATGAGGCTTGGTTGTTTTTTAA 243

Qy   1251 GTATTGATGAACTGTAAATTTATTTATTATAGGATAAATTT 1290
          | ||- | |||| ||| |||||||||||
Db   242 ATTTTTTCTATTTCTATTATTTTCTATCGAATTATTTTT 203

Search completed: September 11, 2005, 02:57:38
Job time : 259.949 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 02:51:01 ; Search time 1002.55 Seconds
(without alignments)
8568.071 Million cell updates/sec

Title: US-10-632-436A-1
Perfect score: 1308
Sequence: 1 gtatacatatacacaacata........ttaaaagggtacttagat 1308

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1308	100.0	1308	18	US-10-632-436A-1	Sequence 1, Appli
2	1278	97.7	1325	18	US-10-425-114-14526	Sequence 14526, A
3	1255	95.9	1281	10	US-09-533-029-65	Sequence 65, Appl
4	1255	95.9	1281	10	US-09-934-455-15	Sequence 15, Appl
5	1255	95.9	1281	14	US-10-278-173-3	Sequence 3, Appli
6	1255	95.9	1281	15	US-10-295-403-17	Sequence 17, Appl
7	1255	95.9	1281	15	US-10-278-536-23	Sequence 23, Appl
8	1255	95.9	1281	17	US-10-225-068-137	Sequence 137, App
9	1255	95.9	1281	17	US-10-225-066A-795	Sequence 795, App
10	1255	95.9	1281	17	US-10-374-780A-169	Sequence 169, App
11	1255	95.9	1281	18	US-10-412-699B-579	Sequence 579, App
12	1255	95.9	1281	18	US-10-685-922-1	Sequence 1, Appli
13	1255	95.9	1281	21	US-10-225-068-137	Sequence 137, App
14	1255	95.9	1281	22	US-10-225-066A-795	Sequence 795, App
15	1035	79.1	1035	9	US-09-938-842A-2316	Sequence 2316, Ap
16	1035	79.1	1035	11	US-09-938-842A-2316	Sequence 2316, Ap
17	1035	79.1	1035	22	US-10-996-058-35	Sequence 35, Appl
18 c	971.8	74.3	1003	9	US-09-770-445-229	Sequence 229, Appl
19	517.8	39.6	1002	22	US-10-996-058-37	Sequence 37, Appl
20	517.8	39.6	1078	18	US-10-425-114-14556	Sequence 14556, A
21	517.8	39.6	1155	10	US-10-934-455-35	Sequence 35, Appl
22	517.8	39.6	1155	17	US-10-225-068-77	Sequence 77, Appl
23	517.8	39.6	1155	17	US-10-225-066A-419	Sequence 419, App
24	517.8	39.6	1155	17	US-10-225-067-31	Sequence 31, Appl
25	517.8	39.6	1155	17	US-10-374-780A-369	Sequence 369, App
26	517.8	39.6	1155	18	US-10-412-699B-1891	Sequence 1891, Ap
27	517.8	39.6	1155	18	US-10-685-922-7	Sequence 7, Appli
28	517.8	39.6	1155	21	US-10-225-068-77	Sequence 77, Appl
29 c	517.8	39.6	1155	22	US-10-225-066A-419	Sequence 419, App
30	493.8	37.8	969	18	US-10-685-922-41	Sequence 41, Appl
31	389.8	29.8	1239	9	US-09-810-836B-1	Sequence 1, Appli
32	389.8	29.8	1239	10	US-09-934-455-413	Sequence 413, App
33	389.8	29.8	1239	14	US-10-278-173-5	Sequence 5, Appli
34	389.8	29.8	1239	15	US-10-295-403-35	Sequence 35, Appl
35	389.8	29.8	1239	17	US-10-225-066A-577	Sequence 577, App
36	389.8	29.8	1239	17	US-10-374-780A-2071	Sequence 2071, Ap
37	389.8	29.8	1239	18	US-10-412-699B-1827	Sequence 1827, Ap
38	389.8	29.8	1239	18	US-10-685-922-5	Sequence 5, Appli
39	389.8	29.8	1239	22	US-10-225-066A-577	Sequence 577, App
40	378.4	28.9	1246	10	US-09-934-455-345	Sequence 345, App
41	378.4	28.9	1246	14	US-10-278-173-123	Sequence 123, App
42	378.4	28.9	1246	15	US-10-295-403-7	Sequence 7, Appli
43	378.4	28.9	1246	15	US-10-278-536-171	Sequence 171, App
44	378.4	28.9	1246	17	US-10-225-066A-587	Sequence 587, App
45	378.4	28.9	1246	17	US-10-374-780A-1949	Sequence 1949, Ap

ALIGNMENTS

RESULT 1
US-10-632-436A-1
; Sequence 1, Application US/10632436A
; Publication No. US20040078852A1
; GENERAL INFORMATION:
; APPLICANT: Michael F. Thomashow
; APPLICANT: Sarah George Fowler
; APPLICANT: Jonathan Vogel
; APPLICANT: Daniel Zarka
; TITLE OF INVENTION: Transcription Factors to Improve Plant Stress Tolerance
; FILE REFERENCE: 21835-00004
; CURRENT APPLICATION NUMBER: US/10/632,436A
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/400,777
; PRIOR FILING DATE: 2002-08-02
; SEQ ID NO 1
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: This is a cDNA sequence derived from mRNA encoding the putative
; OTHER INFORMATION: AP2 domain transcription factor RAV1 (locus tag: At1g13260).
; OTHER INFORMATION: The RAV1 coding sequence consists of nucleotides 92 through 1126
; OTHER INFORMATION: numbered below.
US-10-632-436A-1

Query Match   100.0%; Score 1308; DB 18; Length 1308;

Best Local Similarity 100.0%; Pred. No. 6.3e-294;
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 GTATACATATACACAACTAATTCACAACACACACAACACAATTTCGTTTTCTTCCATT 60
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Qy   61 GTTTCAAACCATAAAAAAAAAACAGATTAAATGGAATCGAGTAGCGTTGATGAGAGTAC 120
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Db   61 GTTTCAAACCATAAAAAAAAAACAGATTAAATGGAATCGAGTAGCGTTGATGAGAGTAC 120

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Db  121 TACAAGTACAGGTTCCATCTGTGAAACCCCGCGATAACTCCCGCGAAAAGTCGTCGGT 180

Qy  181 AGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCGT 240
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Db  421 CGCCGTCACAAATTTCAAAGACGTGAAGATGACGAGGACGAGGTCGATTTCTTGAATTC 480

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Qy  721 AGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTT 780
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Db  721 AGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTT 780

Qy  781 TGAGGACGTTAACGGGAAAGTGTGGAAGTGTGGAGGCAGGTCGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG 840
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Db  901 CGTTGGTTAGTTTGCAGTTAGTGGATCTAACGGTCAGATCAACAGTTGTACATTGGGGTGGAAGTC 960

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RESULT 2
US-10-425-114-14526
; Sequence 14526, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14526
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB22-009-A10_FLI
US-10-425-114-14526

Query Match 97.7%; Score 1278; DB 18; Length 1325;
Best Local Similarity 100.0%; Pred. No. 6.1e-287;
Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    1 CAACACAAACACATTTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAACACAGATTA 60

Qy   91 AATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAAGTACCATCGTGAAACCCC 150
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Qy  151 GGGGATAACTCCGCGGAAAAGTCGTCCGTCGGTAGTAACTTATACAGGATGGGATGGGAAGCGGATC 210
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Db  121 GGGGATAACTCCGCGGAAAAGTCGTCCGTCGGTAGTAACTTATACAGGATGGGATGGGAAGCGGATC 180

Qy  211 AAGCGTTGTTAGATTCAGAGAACGGCCAACAAACCGAAGATGGGGAGCTTCCGTCGTC 270
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Db  181 AAGCGTTGTTAGATTCAGAGAACGGCCAACAAACCGAAGATGGGGAGCTTCCGTCGTC 240

Qy  271 AAAATACAAAGCGTGTGCCACAAACCAAACGGAAGATGGGGAGCTTCAGATTTACGAGAA 330
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Qy  331 ACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAGAGCAGCCGCTCGTGCCTACGA 390
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Qy  391 CGTCGCCGGTTCACAGGTTCCGTCGCCGGATTCCGGGAAACAAAGAGTGAACGATACTGAGAAGAT 450
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; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne

; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G867
US-09-533-029-65

Query Match   95.9%; Score 1255; DB 10; Length 1281;
Best Local Similarity   99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCGTGAAACC 148
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Qy  149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGAAGCGGA 208
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Qy  209 TCAAGCGTTGTTGTTAGATTCAGAGACAACGGGCTAGAGCGTGAATCTAGGAGCTTCCGTCG 268
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Db  181 TCAAGCGTTGTTGTTAGATTCAGAGACAACGGGCTAGAGCGTGAATCTAGGAGCTTCCGTCG 240

Qy  269 TCAAAATACAAAGGTGTGGTGCCAACCAAACGAAGATGGGAGCTCAGATTTACGAG 328
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Db  241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAG 300

Qy  329 AAACACCAGCGCGTGGCTCGGGACATTCAACGAAGAAGCAGAGCGCGCTCGTCGTCGTAC 388
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Db  301 AAACACCAGCGCGTGGCTCGGGACATTCAACGAAGAAGCAGAGCGCGCTCGTCGTCGTAC 360

Qy  389 GACGTCGCGGTTCACAGGTTCCGTGCCGTCACAAATTTCAAAGACGTGAAG 448
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Db  361 GACGTCGCGGTTCACAGGTTCCGTGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy  449 ATGGACGAAGCAGAGCGAGGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATATG 508
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Qy  509 TTGAGGAAACATACTTATAACGAAGAGTTAGACGTCGGGGTTGAGTAATGGTAAC 568
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Db  481 TTGAGGAAACATACTTATAACGAAGAGTTAGACGTCGGGGTTGAGTAATGGTAAC 540

Qy  569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
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Db  541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy  629 GGGTTTAGATCGGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
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Db  601 GGGTTTAGATCGGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660
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Db  361 CGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCTGAATTCAAAATTCAAAGACGTGATAGAT 420
Qy  451 GGACGAAGCAGAGCGAGTCGATTTCTTCATTCGAAATCTCGAATATCTGATATGTT 510
Db  421 GGACGAAGCGAGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATATGTT 480
Qy  511 GAGGAAACATACTTATAACGAAGAGTTAGACGGCGTCGTAATGGTAACGG 570
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Qy  571 AAACATGACTAGGACGTTGTTGAGTAATGATGGTGTTTCTACGACGGG 630
Db  541 AAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGG 600
Qy  631 GTTTAGATCGGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCT 690
Db  601 GTTTAGATCGGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCT 660
Qy  691 AAACCGTTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGTAA 750
Db  661 AAACCGTTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGTAA 720
Qy  751 CGTTTCCCGTGAAAGGAGTGTTGTTGAACTTGACGGACGTTAACGGGAAAGTGTGGAGGTT 810
Db  721 CGTTTCCCGTGAAAGGAGTGTTGTTGAACTTGACGGACGTTAACGGGAAAGTGTGGAGGTT 780
Qy  811 CCGGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTT 870
Db  781 CCGGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTT 840
Qy  871 CGTTAAGGAGAAGAATCTACGTGCTGGTGACGTCGTTAGTTTCAGTAGATCTAACGGTCA 930
Db  841 CGTTAAGGAGAAGAATCTACGTGCTGGTGACGTCGTTAGTTTCAGTAGATCTAACGGTCA 900
Qy  931 GGATCAACAGTTGTACATTGGGTCGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCG 990
Db  901 GGATCAACAGTTGTACATTGGGTCGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCG 960
Qy  991 GGTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGTTCAAGACAACGACGTCGTAGG 1050
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Db 1021 AAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAGCAACGCAT 1080
Qy 1111 CTTTCACGCGCCTCGTAACAACTCTTCTTCTTTTTGTTTGTTTTAATAATTTT 1170
Db 1081 CTTTCACGCGCCTCGTAACAACTCTTCTTCTTTTTGTTTGTTTTAATAATTTT 1140
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Db 1141 TAAAAACTCCATTTCGTTTTCTTATTTGCATCGGTTTCTTCTTGTTTACCAAAG 1200
Qy 1231 GTTCATGAGTTGTTTTGTTGTGTGTATTGATGAACTGTAAATTTATTTATTATAGGATAAATTTT 1290
Db 1201 GTTCATGAGTTGTTTTGTTGTGTGTATTGATGAACTGTAAATTTATTTATTATAGGATAAATTTT 1260
Qy 1291 AAAAAGGGTTACTTAGAT 1308
Db 1261 AAAAAGGGTTACTTAGAT 1278
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; APPLICANT: Heard, Jacqueline
; APPLICANT: Brown, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James

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;    SOFTWARE: PatentIn version 3.1
;    SEQ ID NO 15
;    LENGTH: 1281
;    TYPE: DNA
;    ORGANISM: Arabidopsis thaliana
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (64)..(1098)
;    OTHER INFORMATION: G867
US-09-934-455-15

Query Match          95.9%;    Score 1255;   DB 10;   Length 1281;
Best Local Similarity   99.9%;    Pred. No. 1.3e-281;
Matches 1266;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;
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Qy    29  CACAACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAACACAGAT  88
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Db     1  CACAACAAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT  60

Qy    89  TAAATGGAATCGAGTAGCGTTGATGAGTAGTACACAGTACTACACAGGTTCCATCTGTGAAACC  148
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Db    61  TAAATGGAATCGAGTAGCGTTGATGAGTAGTACACAGTACTACACAGGTTCCATCTGTGAAACC  120

Qy   149  CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTAATACAGGATGGGAAGCCGA  208
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Db   181  TCAAGCGGTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  240

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Qy   389  GACGTCGCGGTTCACAGGTTCCGTCGCGCCGTCGACGCCGTCACAAATTCAAAGACGTGAAG  448
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Db   361  GACGTCGCGGTTCACAGGTTCCGTCGCGCCGTCGACGCCGTCACAAATTCAAAGACGTGAAG  420

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Db   481  TTGAGGAAACATACTACTTATAACGAAGAGTTAGAGCAGAGTAGCCGTCGTAATGGTAAC  540

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Db   601  GGGTTTGAGTCGGCGAGGCACTGTTTGAGAAAGCGGTAACCGTCGGGAAGCGGTTGGGAAG  660

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Db   661  CTAAACCGTTGGTTATACCGTCAGTGGTAGTCGTTGGTGCTCGTTACGACGGAAAGTGTGGAGG  720

Qy   749  AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAGGAAAGTGTGGAGG  808
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Db   721  AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAGGAAAGTGTGGAGG  780

Qy   809  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTCAGTTTGACTAAAGGTTGGAGCAGG  868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG  840

Qy   869  TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGCGTGGTTCAGTAGTTCAGTTGATCTAACGGT  928
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Db   841  TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGCGTGGTTAGTTTTCAGTAGTTCAGTTGATCTAACGGT  900

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Db   901  CAGGATCAACAGTTGTACATTGGGTGGAGTCGAGATCGGTCAGATTTAGATGCGGGT  960

Qy   989  CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACAACGACGTCGTA  1048
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Db   961  CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACAACGACGTCGTA  1020

Qy  1049  GGAAACAAAAGAGTGAACGACGTCGAGATGTTATCGTCGGTGGTCGTAGGAGAGCAACGC  1108
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Db  1021  GGAAACAAAAGAGTGAACGACGTGAACGATACTGAGATGTTATCGTCGGTGGTCGTAGCAAGAGAGCAACGC  1080

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RESULT 4
US-09-934-455-15
;    Sequence 15, Application US/09934455
;    Publication No. US20030121070A1
;    GENERAL INFORMATION:
;    APPLICANT: Adam, Luc
;    APPLICANT: Creelman, Robert
;    APPLICANT: Dubell, Arnold
;    APPLICANT: Heard, Jacqueline
;    APPLICANT: Jiang, Cai-Zhong
;    APPLICANT: Keddie, James
;    APPLICANT: Pilgrim, Marsha
;    APPLICANT: Ratcliffe, Oliver
;    APPLICANT: Reuber, Lynne
;    APPLICANT: Riechmann, Jose Luis
;    APPLICANT: Yu, Guo-Liang
;    APPLICANT: Pineda, Omaira
;    TITLE OF INVENTION: Genes for Modifying Plant Traits IV
;    FILE REFERENCE: MBI-0025
;    CURRENT APPLICATION NUMBER: US/09/934,455
;    CURRENT FILING DATE:  2001-08-22
;    PRIOR APPLICATION NUMBER: 60/227439
;    PRIOR FILING DATE: 2000-08-22
;    PRIOR APPLICATION NUMBER: MBI-0022
;    PRIOR FILING DATE: 2001-11-16
;    PRIOR APPLICATION NUMBER: MBI-0023
;    PRIOR FILING DATE: 2001-04-17
;    NUMBER OF SEQ ID NOS: 516
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Db   361  GACGTCGCGGTTCCGTCGCCGCCGCGGTCACAGTTCACAAATTTCAAAGAGCTGAAG      420

Qy   449  ATGGACGAAGACAGGTCGATTCTCATTCGAAATCTGAGATCGTTGATATG            508
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Db   421  ATGGACGAAGACAGGTCGATTCTCATTCGAAATCTGAGATCGTTGATATG            480

Qy   509  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC  568
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Db   601  GGGGTTTAGATCGGCGGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

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Db  1081  ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTCTTTTGTTGTTTTAATAATT    1139

Qy  1169  TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCTTCTTCTTCTTGTTTACCAA    1228
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Db  1140  TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCTTCTTCTTCTTGTTTACCAA    1199

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Db  1260  TTAAAAA  1266
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Query Match             95.9%;  Score 1255;  DB 14;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 1.3e-281;
Matches 1266;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy    29  CACAACACAAACACATTCTGTTTCTCCATTGTTTCAACCATAAAAAAAAACACAGAT      88
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Qy  209  TCAAGCGTGTGTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  268
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Db  181  TCAAGCGTGTGTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  240

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Db  241  TCAAAATACAAAGGTGTGGTGCCACCAAACGGAGAGATGGGAGCTCAGATTTAGCAGAG  300

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Db  301  AAACACCAGCGCGTGTGCTCGGGACATTCAACGAGAAGACGAAGCCGCTCGTGCCTAC  360

Qy  389  GACGTCGGGGTTCACAGTTCCGTCGCCGTGACGCCGTCACAAATTCACAAAGACGTGAAG  448
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Qy  449  ATGGACGAAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG  508
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Db  721  AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAGG  780

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Qy  929  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGAGTGCGGGT  988
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RESULT 6

US-10-295-403-17

; Sequence 17, Application US/10295403
; Publication No. US20030101481A1

GENERAL INFORMATION:

;   APPLICANT: Heard, Jacqueline
;   APPLICANT: Riechmann, Jose Luis
;   APPLICANT: Adam, Luc
;   APPLICANT: Broun, Pierre
;   APPLICANT: Pineda, Omaira
;   APPLICANT: Reuber, Lynne
;   APPLICANT: Jiang, Cai-Zhong
;   APPLICANT: Keddie, James
;   APPLICANT: Zhang, James
;   APPLICANT: Benito, Maria-Ines
;   APPLICANT: Yu, Guo-Liang
;   APPLICANT: Fromm, Mike

;   TITLE OF INVENTION: PLANT GENE SEQUENCES I
;   FILE REFERENCE: MBI-0003
;   CURRENT APPLICATION NUMBER: US/10/295,403
;   CURRENT FILING DATE: 2002-11-15
;   PRIOR APPLICATION NUMBER: US/09/394,519
;   PRIOR FILING DATE: 1999-09-13
;   PRIOR APPLICATION NUMBER: 60/101,349
;   PRIOR FILING DATE: 1998-09-22
;   PRIOR APPLICATION NUMBER: 60/103,312
;   PRIOR FILING DATE: 1998-10-06
;   PRIOR APPLICATION NUMBER: 60/108,734
;   PRIOR FILING DATE: 1998-11-12
;   PRIOR APPLICATION NUMBER: 60/113,409
;   PRIOR FILING DATE: 1998-12-22
;   NUMBER OF SEQ ID NOS: 170
;   SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)..(1095)
;   OTHER INFORMATION: G867

US-10-295-403-17

Query Match   95.9%; Score 1255; DB 15; Length 1281;
Best Local Similarity   99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Db  1    CACACACAAACAACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT  60

Qy  89   TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC  148
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Db  61   TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC  120

Qy  149  CCGGCGATAACTCCGGCGAAAAAGTCGTCGTAGGTAACTTATACAGGATGGGAAGCGGA  208
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CCGGCGATAACTCCGGCGAAAAAGTCGTCGTAGGTAACTTATACAGGATGGGAAGCGGA  180
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Db 1260 TTAAAAA 1266
         |||||||
Qy 1260 TTAAAAA 1266

RESULT 7
US-10-278-536-23
; Sequence 23, Application US/10278536
; Publication No. US20030131386A1
GENERAL INFORMATION:
; APPLICANT: Samaha, Raymond
; APPLICANT: Heard, Jacqueline
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Keddie, James
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Adam, Luc
; APPLICANT: Broun, Pierre
; TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-011
; CURRENT APPLICATION NUMBER: US/10/278,536
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G867
US-10-278-536-23

Query Match   95.9%; Score 1255; DB 15; Length 1281;
Best Local Similarity   99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy   29 CACACACAAACACATTTCGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 88
         ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1 CACACACAAACACATTTCGTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 148
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 120

Qy 149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAGCGGA 208
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAGCGGA 180

Qy 209 TCAAGCGTTGTTGTTAGATTCAGAGAACGGCGGCTAGAGAGCTGAATCTAGGAGAGCTTCCGTCG 268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 TCAAGCGTTGTTGTTAGATTCAGAGAACGGCGGCTAGAGAGCTGAATCTAGGAGAGCTTCCGTCG 240

Qy 269 TCAAAATACAAAGGTGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTACGAG 328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TCAAAATACAAAGGTGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTACGAG 300

Qy 329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 388
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 360

Qy 389 GACGTTCGCGGTTCACAGGTTCCGTCGCCGTGACGCGTCACAAATTTCAAAGACGTGAAG 448
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GACGTTCGCGGTTCACAGGTTCCGTCGCCGTGACGCGTCACAAATTTCAAAGACGTGAAG 420

Qy 449 ATGGACGAAGACGAGGTCGATTTCTCATTCGAATTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 508
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 ATGGACGAAGACGAGGTCGATTTCTCATTCGAATTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy 509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAGTAAACGGCTGCGTAATGGTAAC 568
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAGTAAACGGCTGCGTAATGGTAAC 540

Qy 569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
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Db 541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy 629 GGGTTAGATCGGCGGAGGCACTGTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAAG 688
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 GGGTTAGATCGGCGGAGGCACTGTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAAG 660

Qy 689 CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy 749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy 809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy 869 TTCGTTAAGGAGAAATCTACGTGCTCGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 TTCGTTAAGGAGAAATCTACGTGCTCGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy 929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGGT 988
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGGT 960

Qy 989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy 1049 GGAAACAAAAGAGTGAACGAATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1108
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GGAAACAAAAGAGTGAACGAATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1080

Qy 1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTCTTTTGTTTGTTTAATAATT 1168
         |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db 1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTTCTTTTGTTTGTTTAATAATT 1139

Qy 1169 TTTAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCATCTGTTTACCAA 1228
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1140 TTTAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCATCTGTTTACCAA 1199

Qy 1229 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1200 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy 1289 TTAAAAA 1295
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Db 1260 TTAAAAA 1266

RESULT 8
US-10-225-068-137
; Sequence 137, Application US/10225068
; Publication No. US20030217383A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Adam, Luc J.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Broun, Pierre E.

```
;   TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
;   TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
;   FILE REFERENCE: 51442002040
;   CURRENT APPLICATION NUMBER: US/10/225,068
;   CURRENT FILING DATE:  2002-08-09
;   PRIOR APPLICATION NUMBER: 60/310,847
;   PRIOR FILING DATE: 2001-08-09
;   PRIOR APPLICATION NUMBER: 60/336,049
;   PRIOR FILING DATE: 2001-11-19
;   PRIOR APPLICATION NUMBER: 60/338,692
;   PRIOR FILING DATE: 2001-12-11
;   PRIOR APPLICATION NUMBER: 10/171,468
;   PRIOR FILING DATE: 2002-06-14
;   NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 137
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1098)
US-10-225-068-137

  SOFTWARE: FastSEQ for Windows Version 4.0

Query Match             95.9%;  Score 1255;  DB 17;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 1.3e-281;
Matches 1266;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;

Qy          29 CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 88
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 60

Qy          89 TAAATGGAATCGAGTAGGTTGATGAGAGTACTACAGAGTTCCATCTGTGAAACC 148
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TAAATGGAATCGAGTAGGTTGATGAGAGTACTACAGAGTTCCATCTGTGAAACC 120

Qy         149 CCGGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CCGGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy         209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTGAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTGAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy         269 TCAAAATACAAAGGTGTGTGCCACAACCAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCAAAATACAAAGGTGTGTGCCACAACCAACCAAACGGAAGATGGGGAGCTTCAGATTTACGAG 300

Qy         329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGAAGAGCCGCTCGTCGCCTAC 388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGAAGAGCCGCTCGTCGCCTAC 360

Qy         389 GACGTCGCCGTTCACAGGTTCCGTCGCGCCGTGACGCCGTTCACAAATTTCAAAGACGTGAAG 448
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GACGTCGCCGTTCACAGGTTCCGTCGCGCCGTGACGCCGTTCACAAATTTCAAAGACGTGAAG 420

Qy         449 ATGACGAAGACGAGGTCGATTCTTCATTCGAAATCTGAGATCGTTGATATG 508
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATGACGAAGACGAGGTCGATTCTTCATTCGAAATCTGAGATCGTTGATATG 480

Qy         509 TTGAGGGAAACATACTTATAACGAAGAGTTAGACGCAGAGTAAACGGCCGTCGTAATGGTAAC 568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TTGAGGGAAACATACTTATAACGAAGAGTTAGACGCAGAGTAAACGGCCGTCGTAATGGTAAC 540

Qy         569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy         629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGGCCAAGCGACGTTGGGAAG 688
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGGTTTAGATCGGCGGAGCACTGTTTGAGAAAGCGGTAACGGCCAAGCGACGTTGGGAAG 660

Qy         689 CTAAACCGTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CTAAACCGTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy         749 AACGTTTCCGTGAAAGGAGTGTGTTGTGAACTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 AACGTTTCCGTGAAAGGAGTGTGTTGTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy         809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTTTGACTAAAGGTTCGGAGCAGG 868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTTTGACTAAAGGTTCGGAGCAGG 840

Qy         869 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTGAGTTTCAGTAGATCTAACGGT 928
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTGAGTTTCAGTAGATCCTAACGT 900

Qy         929 CAGGATCAACAGTTGTACATTGGGTGGAAGTTAACATTCACCGGAGAGTTCAAGAAAACGACGTCGTA 988
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 CAGGATCAACAGTTGTACATTGGGTGGAAGTTAACATTCACCGGAGAGTTCAAGAAAACGACGTCGTA 960

Qy         989 CGGGTTTGAGATTGTTCGGAGTTAACATTTCTTATTGCATCGGTTCTTCTTCTCTGTTTACCAA 1048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CGGGTTTGAGATTGTTCGGAGTTAACATTTCTTATTGCATCGGTTCTTCTTCTCTGTTTACCAA 1020

Qy        1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGGTAGCAAGAAGCAACGC 1108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGGTAGCAAGAAGCAACGC 1080

Qy        1109 ATCTTTCACGCCCGTAACAACTCCTCTTCTTCTTTCTTTTTTCTTTTGTTTGTTTTAATAATT 1168
               |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        1081 ATCTTTCACGCCTCGTAACAACTCTCTTC-TTTTTTTCTTTGTTTGTTTTAATAATT 1139

Qy        1169 TTTAAAAACTCCATTTCGTTTTCTTATTGCATCGGTTCTTCTCTGTTTACCAA 1228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1140 TTTAAAAACTCCATTTCGTTTTCTTATTTGCATCGGTTCTTCTCTGTTTACCAA 1199

Qy        1229 AGGTTCATGAGTTGTTTTGTTGTATTGATGAGAACTGTAAATTTATTTATAGGATAAATT 1288
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1200 AGGTTCATGAGTTGTTTTGTTGTATTGATGAGAACTGTAAATGTAAATTTTATTTATAGAGATAAATT 1259

Qy        1289 TTAAAAA 1295
               |||||||
Db        1260 TTAAAAA 1266


RESULT 9
US-10-225-066A-795
; Sequence 795, Application US/10/225,066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
;   APPLICANT: Mendel Biotechnology, Inc.
;   APPLICANT: RATCLIFFE, Oliver
;   APPLICANT: RIECHMANN, Jose Luis
;   APPLICANT: ADAM, Luc J
;   APPLICANT: DUBELL, Arnold T
;   APPLICANT: HEARD, Jacqueline E
;   APPLICANT: PILGRIM, Marsha L
;   APPLICANT: JIANG, Cai-Zhong
;   APPLICANT: REUBER, T. Lynne
;   APPLICANT: CREELMAN, Robert A
;   APPLICANT: PINEDA, Omaira
;   APPLICANT: YU, Guo-Liang
;   APPLICANT: BROUN, Pierre E
;   TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
;   FILE REFERENCE: MBI0036-2 US
;   CURRENT APPLICATION NUMBER: US/10/225,066A
;   CURRENT FILING DATE:  2002-08-09
;   PRIOR APPLICATION NUMBER: 09/837,444
;   PRIOR FILING DATE: 2001-04-18
;   PRIOR APPLICATION NUMBER: 60/310,847
;   PRIOR FILING DATE: 2001-08-09
;   PRIOR APPLICATION NUMBER: 60/336,049
;   PRIOR FILING DATE: 2001-12-05
;   PRIOR APPLICATION NUMBER: 60/338,692
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;   PRIOR FILING DATE: 2001-12-11
;   PRIOR APPLICATION NUMBER: 10/171,468
;   PRIOR FILING DATE: 2002-06-14
;   NUMBER OF SEQ ID NOS: 1122
;   SOFTWARE: PatentIn version 3.1
SEQ ID NO 795
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-225-066A-795

Query Match         95.9%;   Score 1255;  DB 17;   Length 1281;
Best Local Similarity 99.9%;  Pred. No. 1.3e-281;
Matches 1266;  Conservative  0;   Mismatches  0;   Indels  1;   Gaps  1;

Qy          29 CACAACAAACACATTTCTGTTTTCCCATTGTTCAAACCATAAAAAAAAACACAGAT 88
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 CACAACAAACACATTTCTGTTTTCCCATTGTTCAAACCATAAAAAAAAACACAGAT 60

Qy          89 TAAATGGAATCGAGTAGCGTTGATGAGTACTACAGAGTTCCATCTGTGAAACC 148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TAAATGGAATCGAGTAGCGTTGATGAGTACTACAGAGTTCCATCTGTGAAACC 120

Qy         149 CCGGGCGATAACTAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGA 208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CCGGGCGATAACTAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGA 180

Qy         209 TCAAGCGTTGTGTTGTAGATTCAGAGAACGGCGTAGAAGCTGAATCTGAGAAGCTTCCGTCG 268
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TCAAGCGTTGTGTTGTAGATTCAGAGAACGGCGTAGAAGCTGAATCTGAGAAGCTTCCGTCG 240

Qy         269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGAATGGGGAGCTCAGATTTACGAG 328
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGAATGGGGAGCTCAGATTTACGAG 300

Qy         329 AAACACCAGCGCGCCGTGCTGCCTCCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AAACACCAGCGCGCCGTGCTGCCTCCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 360

Qy         389 GACGTCGCGGTTCACAGTTCCGTCGCCGTGAGCGCCGTCACAAATTTCAAAGACGTGAAG 448
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GACGTCGCGGTTCACAGTTCCGTCGCCGTGAGCGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy         449 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy         509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy         569 GGAAACATGACTAGGACGGTTGTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GGAAACATGACTAGGACGGTTGTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy         629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy         689 CTAAACCGTTTGGTTATACCGGAAACATCACGCGAGAAACATTTCCGTTACCGTCAAGT 748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CTAAACCGTTTGGTTATACCGGAAACATCACGCGAGAAACATTTCCGTTACCGTCAAGT 720

Qy         749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAGG 808
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAGG 780

Qy         809 TTCCGTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 TTCCGTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy         869 TTCGTTAAGGAGAGAGAATCTACGTCGTCGGTGACGTGGTAGTTTCAGTAGATCTAACGGT 928
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TTCGTTAAGGAGAGAGAATCTACGTCGTCGGTGACGTGGTAGTTTCAGTAGATCTAACGGT 900

Qy         929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCGGGTCAGATTTAGATGCGGGT 988
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCGGGTCAGATTTAGATGCGGGT 960

Qy         989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy        1049 GGAAACAAAAGAGTGAACGATACTGAGATGTATCGTTCGGTGGTTGGTTGTGGTCAAGAGCAACGC 1108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GGAAACAAAAGAGTGAACGATACTGAGATGTATCGTTCGGTGGTTGGTTGTGGTCAAGAGCAACGC 1080

Qy        1109 ATCTTTCACGCCTCGTAACAACTCTTCTCTC-TTTTTTTCTTTTGTGTTTGTTTGTTTAATAATT 1168
               |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        1081 ATCTTTCACGCCTCGTAACAACTCTTCTC-TTTTTTTCTTTTGTGTTTGTTTGTTTAATAATT 1139

Qy        1169 TTTAAAACTCCATTTCGTTTCTTATTTGCATCGGTTTCTTCTTCTTCTTGTTTACCAA 1228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1140 TTTAAAACTCCATTTCCTTTCTTATTTGCATCGGTTTCTTCTTCTTCTTGTTTACCAA 1199

Qy        1229 AGGTTCATGAGTGTGTTTTGTTGGTATTGATTGAACTGTAAATTTTATTTATAGGATAAATT 1288
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1200 AGGTTCATGAGTGTGTTTTGTTGGTATTGATTGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy        1289 TTAAAAA 1295
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Db        1260 TTAAAAA 1266


RESULT 10
US-10-374-780A-169
;   Sequence 169, Application US/10374780A
;   Publication No. US20040019927A1
;   GENERAL INFORMATION:
;   APPLICANT: Sherman, Bradley K
;   APPLICANT: Riechmann, Jose Luis
;   APPLICANT: Jiang, Cai-Zhong
;   APPLICANT: Heard, Jacqueline E
;   APPLICANT: Haake, Volker
;   APPLICANT: Creelman, Robert A
;   APPLICANT: Ratcliffe, Oliver
;   APPLICANT: Adam, Luc J
;   APPLICANT: Reuber, T. Lynne
;   APPLICANT: Keddie, James
;   APPLICANT: Broun, Pierre B
;   APPLICANT: Pilgrim, Marsha L
;   APPLICANT: Dubell III, Arnold T
;   APPLICANT: Pineda, Omaira
;   APPLICANT: Yu, Guo-Liang
;   TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
;   FILE REFERENCE: MBI-0047 CIP
;   CURRENT APPLICATION NUMBER: US/10/374,780A
;   CURRENT FILING DATE: 2003-02-25
;   PRIOR APPLICATION NUMBER: 09/837,944
;   PRIOR FILING DATE: 2001-04-18
;   PRIOR APPLICATION NUMBER: 60/310,847
;   PRIOR FILING DATE: 2001-08-09
;   PRIOR APPLICATION NUMBER: 09/934,455
;   PRIOR FILING DATE: 2001-08-22
;   PRIOR APPLICATION NUMBER: 60/336,049
;   PRIOR FILING DATE: 2001-11-19
;   PRIOR APPLICATION NUMBER: 60/338,692
;   PRIOR FILING DATE: 2001-12-11
;   PRIOR APPLICATION NUMBER: 10/171,468
;   PRIOR FILING DATE: 2002-06-14
;   PRIOR APPLICATION NUMBER: 10/225,066
;   PRIOR FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: 10/225,067
;   PRIOR FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: 10/225,068
;   PRIOR FILING DATE: 2002-08-09
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;   NUMBER OF SEQ ID NOS: 2906
;   SOFTWARE: PatentIn version 3.2
;
;   SEQ ID NO 169
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   OTHER INFORMATION: G867
US-10-374-780A-169

Query Match      95.9%;   Score 1255;   DB 17;   Length 1281;
Best Local Similarity   99.9%;   Pred. No. 1.3e-281;
Matches 1266;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;

Qy      29  CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT    88
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT    60

Qy      89  TAAATGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACCAGGTTCCATCTGTGAAACC   148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  TAAATGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACCAGGTTCCATCTGTGAAACC   120

Qy     149  CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCGGA   208
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCGGA   180

Qy     209  TCAAGCGGTTGTGTTAGATTCAGAGAACGGCCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG   268
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  TCAAGCGGTTGTGTTAGATTCAGAGAACGGCCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG   240

Qy     269  TCAAAATACAAAGGTGGTGCCACAACCAAACGGAAGAGATGGGAGCTCAGATTTACGAAG   328
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     241  TCAAAATACAAAGGTGGTGCCACAACCAAACGGAAGAGATGGGAGCTCAGATTTACGAG    300

Qy     329  AAACACCAGCGCGGTGGCTCGGACATTCAACGAAGAAGACGAAGCGCCGTTCGTCGCCTAC   388
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  AAACACCAGCGCGGTGGCTCGGACATTCAACGAAGAAGACGAAGCGCCGTTCGTCGCCTAC   360

Qy     389  GACGTGCGGTTCACAGGTTCCGTCGACGCCGTCACAAATTTCAAAGACGTGAAG        448
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  GACGTGCGGTTCACAGGTTCCGTCGACGCCGTCACAAATTTCAAAGACGTGAAG        420

Qy     449  ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTCGAAATCGTCGTTGATATG     508
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTCGAAATCGTCGTTGATATG     480

Qy     509  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAACGCGCCGTTCGTAATGTAAC   568
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAACGCGCCGTTCGTAATGTAAC   540

Qy     569  GGAAACATGACTAGGACGTTGTAACGTCGGGTTGAGTAATGATGGTGTTTCTACGACG     628
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  GGAAACATGACTAGGACGTTGTAACGTCGGGTTGAGTAATGATGGTGTTTCTACGACG     600

Qy     629  GGGTTTAGATCGGCGGAGGCACTGTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAG    688
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  GGGTTTAGATCGGCGGAGGCACTGTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAG    660

Qy     689  CTAAACCGTTGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT     748
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CTAAACCGTTGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT     720

Qy     749  AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGTTGAGGACGTTAACGGGAAAGTGTGGAGG  808
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGTTGAGGACGTTAACGGGAAAGTGTGGAGG  780

Qy     809  TTCCGTTACTCGTATTGGAACAGTCGAGTTATGTTTGACTAAAGGTTGGAGCAGG      868
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  TTCCGTTACTCGTATTGGAACAGTCGAGTTATGTTTGACTAAAGGTTGGAGCAGG      840

Qy     869  TTCGTTAAGGAAGAGAATCTACGTGCGTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT   928
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  TTCGTTAAGGAAGAGAATCTACGTGCGTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT   900

Qy     929  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT   988
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT   960

Qy     989  CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA  1048
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA  1020

Qy    1049  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTGTGGTGTAGCAAGAAGCAACGC  1108
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTGTGGTGTAGCAAGAAGCAACGC  1080

Qy    1109  ATCTTTCACGCCTCGTAACAACTCTCTCTTTTTTTTTTGTTGTTTGTTTTAATAATT   1168
            ||||||||||||||||||||||||||||||||| |||||||||  |||||||||||||
Db    1081  ATCTTTCACGCCTCGTAACAACTCTCTCTTC-TTTTTTTTCTTTGTTTGTTTTAATAATT  1139

Qy    1169  TTTAAAACTCCATTTTCGTTTCTTATTTGCATCGGTTTCTTCTTCTTGTTTACCAA   1228
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140  TTTAAAACTCCATTTTCGTTTCTTATTTGCATCGGTTTCTTCTTCTTGTTTACCAA   1199

Qy    1229  AGGTTCATGAGTTGTTTTGTGTTGTGATTGAGATGGTAAATTTTATTTATAGAGATAAATT  1288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200  AGGTTCATGAGTTGTTTTGTGTTGTGATTGAGATGGTAAATTTTATTTATAGAGATAAATT  1259

Qy    1289  TTAAAAA  1295
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Db    1260  TTAAAAA  1266
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RESULT 11
US-10-412-699B-579
;   Sequence 579, Application US/10412699B
;   Publication No. US20040045049A1
;   GENERAL INFORMATION:
;   APPLICANT: Mendel Biotechnology, Inc.
;   APPLICANT: Zhang, James
;   APPLICANT: Fromm, Michael E.
;   APPLICANT: Heard, Jacqueline E.
;   APPLICANT: Riechmann, Jose Luis
;   APPLICANT: Adam, Luc J.
;   APPLICANT: Broun, Pierre E.
;   APPLICANT: Pineda, Omaira
;   APPLICANT: Reuber, T. Lynne
;   APPLICANT: Keddie, James S.
;   APPLICANT: Yu, Guo-Liang
;   APPLICANT: Jiang, Cai-Zhong
;   APPLICANT: Samaha, Raymond R.
;   APPLICANT: Pilgrim, Marsha L.
;   APPLICANT: Creelman, Robert A.
;   APPLICANT: DuBell, Arnold N.
;   APPLICANT: Ratcliffe, Oliver
;   APPLICANT: Kumimoto, Roderick
;   APPLICANT: Sherman, Bradley K.
;   TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
;   FILE REFERENCE: MBI-0048CIP
;   CURRENT APPLICATION NUMBER: US/10/412,699B
;   CURRENT FILING DATE:   2003-04-10
;   PRIOR APPLICATION NUMBER: 09/394,519
;   PRIOR FILING DATE: 1999-09-13
;   PRIOR APPLICATION NUMBER: 09/489,376
;   PRIOR FILING DATE: 2000-01-21
;   PRIOR APPLICATION NUMBER: 09/506,720
;   PRIOR FILING DATE: 2000-02-17
;   PRIOR APPLICATION NUMBER: 09/533,030
;   PRIOR FILING DATE: 2000-03-22
;   PRIOR APPLICATION NUMBER: 09/533,392
;   PRIOR FILING DATE: 2000-03-22
;   PRIOR APPLICATION NUMBER: 09/533,029
;   PRIOR FILING DATE: 2000-03-22
;   PRIOR APPLICATION NUMBER: 09/532,591
;   PRIOR FILING DATE: 2000-03-22
;   PRIOR APPLICATION NUMBER: 09/533,648
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;   PRIOR FILING DATE: 2000-03-22
;   PRIOR APPLICATION NUMBER: 09/713,994
;   PRIOR FILING DATE: 2000-11-16
;   PRIOR APPLICATION NUMBER: 09/819,142
;   PRIOR FILING DATE: 2001-03-27
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 2011
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 579
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   OTHER INFORMATION: G867
US-10-412-699B-579

  Query Match        95.9%;   Score 1255;  DB 18;   Length 1281;
  Best Local Similarity   99.9%;   Pred. No. 1.3e-281;
  Matches 1266;  Conservative     0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy     29 CACACACAAACACATTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAACACAGAT   88
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACACACAAACACATTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAACACAGAT   60

Qy     89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC  148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC  120

Qy    149 CCGGCGATAACTCCGGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGA  208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGGCGATAACTCCGGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGA  180

Qy    209 TCAAGGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAAATCTAGGAAGCTTCCGTCG  268
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCAAGGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAAATCTAGGAAGCTTCCGTCG  240

Qy    269 TCAAAATACAAAGGTGTGTGCCACAACCAACGGAAGATGGGGAGCTCAGATTTACGAG  328
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Db    241 TCAAAATACAAAGGTGTGTGCCACAACCAACCAAACCGGAAGATGGGGAGCTCAGATTTACGAG  300

Qy    329 AAACACCAGCCGCGTCGTGCGGCCTCGGGACATTCAACGAAGAGACGAAGCCCGCTCGTGCCTAC  388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAACACCAGCCGCGTCGTGCGGCCTCGGGACATTCAACGAAGAGACGAAGCCCGCTCGTGCCTAC  360

Qy    389 GACGTCGCCGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG  448
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACGTCGCGCGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACCTGAAG  420

Qy    449 ATGGAAGCAGAAGACGAGGTCGATTCTCATTCCGAATTCTGAAATCTGAGATCGTTGATATG  508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGGACGAAGACGAGGTCGATTCTCATTCCGAATTCTGAAATCTGAGATCGTTGATATG  480

Qy    509 TTGAGGAAACATACTTATAAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC  568
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTGAGGAAACATACTTATAAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC  540

Qy    569 GGAAACATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  628
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGAAACATGACTAGGACGTGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  600

Qy    629 GGGTTTAGATCGGCCGAGGCCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG  688
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGGTTTAGATCGGCCGAGGCCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG  660

Qy    689 CTAAACCGTTTGGTTATACCGAAACATCACCGCAGAGAAACATTTTCCGTTACCGTCAAGT  748
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTAAACCGTTTGGTTATACCGAAACATCACCGCAGAGAAACATTTTCCGTTACCGTCAAGT  720

Qy    749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGGAAAGTGTGGAGG  808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGGAAAGTGTGGAGG  780

Qy    809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTAGTCAGAGTTATGTTTTTGACTAAAGGTTGGAGCAGG  868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTAGTCAGAGTTATGTTTTTGACTAAAGGTTGGAGCAGG  840

Qy    869 TTCGTTAAGGAGAGAATCTACACGTCGTCGGTGACGTGGTAGTTCAGTAGATCTAACGGT  928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTCGTTAAGGAGAGAATCTACACGTCGTCGGTGACGTGGTAGTTCAGTAGATCTAACGGT  900

Qy    929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  960

Qy    989 CGGGTTTTGAGATTGTTCCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA  1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGTTTTGAGATTGTTCCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA  1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAGATGTATCGTTCGTTGGTGTGGTGAGCAAGAACGC  1108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTCGTTGGTGTGGTGAGCAAGAACGC  1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTCTTTTTGTTTTTGTGTTTAATAATT  1168
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTGTCTTTGTGTTTAATAATT  1139

Qy   1169 TTTAAAAACTCCATTTCGTTTCTTCTTATTTGCATCGGTTCTTCTTCTTCGTTGTTACCAA  1228
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 TTTAAAAACTCCATTTCGTTTCTTTTATTTGCATCGGTTCTTCTTCTTCGTTGTTACCAA  1199

Qy   1229 AGGTTCATGAGTTGTTTTTGTTGTTATTGATGAACTGTAAATTTATTTATTATAGGATAAATT  1288
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTTGTTGTTATTGATGAACTGTAAATTTATTTATTATAGGATAAATT  1259

Qy   1289 TTAAAAA  1295
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Db   1260 TTAAAAA  1266


RESULT 12
US-10-685-922-1
;   Sequence 1, Application US/10685922
;   Publication No. US20040098764A1
;   GENERAL INFORMATION:
;    APPLICANT: MENDEL BIOTECHNOLOGY, INC.
;    APPLICANT: HEARD, Jacqueline
;    APPLICANT: RIECHMANN, Jose Luis
;    APPLICANT: CREELMAN, Robert
;    APPLICANT: RATCLIFFE, Oliver
;    APPLICANT: KUMIMOTO, Roderick W
;    APPLICANT: GUTTERSON, Neal
;    APPLICANT: REUBER, T Lynne
;    APPLICANT: PINEDA, Omaira
;    APPLICANT: LIBBY, Jeffrey M
;    APPLICANT: SHERMAN, Bradley K
;    TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
;    FILE REFERENCE: MBI-0049CIP
;    CURRENT APPLICATION NUMBER: US/10/685,922
;    CURRENT FILING DATE: 2003-10-14
;    PRIOR APPLICATION NUMBER: 09/810,836
;    PRIOR FILING DATE: 2001-03-16
;    PRIOR APPLICATION NUMBER: 10/412,699
;    PRIOR FILING DATE: 2003-04-10
;    PRIOR APPLICATION NUMBER: 10/171,468
;    PRIOR FILING DATE: 2002-06-14
;    PRIOR APPLICATION NUMBER: 09/532,591
;    PRIOR FILING DATE: 2000-03-22
;    PRIOR APPLICATION NUMBER: 09/533,029
;    PRIOR FILING DATE: 2000-03-22
;    PRIOR APPLICATION NUMBER: 09/533,392
;    PRIOR FILING DATE: 2000-03-22
;    PRIOR APPLICATION NUMBER: 60/125,814
;    PRIOR FILING DATE: 1999-03-23
;    PRIOR APPLICATION NUMBER: 09/713,994
;    PRIOR FILING DATE: 2000-11-16
;    PRIOR APPLICATION NUMBER: 60/166,228
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;   PRIOR FILING DATE: 1999-11-17
;   PRIOR APPLICATION NUMBER: 09/394,519
;   PRIOR FILING DATE: 1999-09-13
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 64
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 1
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   OTHER INFORMATION: G867 Predicted polypeptide sequence is paralogous to G9, G993, G1
US-10-685-922-1

Query Match      95.9%;   Score 1255;   DB 18;   Length 1281;
Best Local Similarity   99.9%;   Pred. No. 1.3e-281;
Matches 1266;   Conservative    0;   Mismatches    0;   Indels    1;   Gaps    1;

Qy         29 CACAACAAAACACATTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT       88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CACAACAAAACACATTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT       60

Qy         89 TAAATGGAATCGAGTAGCGTTGATGAGTACTACAGAGTACAGGTTCCATCTGTGAAACC      148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TAAATGGAATCGAGTAGCGTTGATGAGTACTACAGAGTACAGGTTCCATCTGTGAAACC      120

Qy        149 CCGGCGATAACTCCGGCGAAAAAGTCGTTCGGTAGGTAACTTATACACGGATGGGAAGCGGA      208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGCGATAACTCCGGCGAAAAAGTCGTTCGGTAGGTAACTTATACACGGATGGGAAGCGGA      180

Qy        209 TCAAGCGTTGTTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG      268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCAAGCGTTGTTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG      240

Qy        269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAG      328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAG      300

Qy        329 AAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGAGACGAAGCGCGCTCGTGCCTAC      388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGAGACGAAGCGCGCTCGTGCCTAC      360

Qy        389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG      448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG      420

Qy        449 ATGGACGAAGACGAGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATATG      508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGACGAAGACGAGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATATG      480

Qy        509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAATGGTAAC      568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAATGGTAAC      540

Qy        569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG      628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG      600

Qy        629 GGGTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTGGGAAG      688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGGTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTGGGAAG      660

Qy        689 CTAAACCGTTGGTTATACCGAAGATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT      748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTAAACCGTTGGTTATACCGAAGACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT      720

Qy        749 AACGTTTCCGTGAAAGAGAGTGTGTTGAACTTTGAACGTTTAACGGGAAAGTGTGGAGG      808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACGTTTCCGTGAAAGAGAGTGTGTTGAACTTTGAACGTTTAACGGACGTGTGGAGCAGG      780

Qy        809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTA      868
              |||||||||||||||||||||||||||||||||||
Db        781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTA      840

Qy        869 TTCGTTAAGGAGGAAGAATCTACGTGCTGCGTGGTGGTGACGTGTGGTTAGTTTCAGTAGATCTAACGGT      928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCGTTAAGGAGGAAGAATCTACGTGCTGCGTGGTGGTGACGTGTGGTTAGTTTCAGTAGATCTAACGGT      900

Qy        929 CAGGATCAACAGTTGTACATTGGGTAGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT      988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGGATCAACAGTTGTACATTGGGTAGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT      960

Qy        989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA     1048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA     1020

Qy       1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCACGC     1108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAAGC     1080

Qy       1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTTCTTTGTTGTTTAATAATT     1168
              ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db       1081 ATCTTTCACGCCTCGTAACAACTCTTCTTCTC-TTTTTTTCTTTGTTGTTTAATAATT     1139

Qy       1169 TTTAAAAACTTCCATTTTCGTTTTCTTATTTGCATCGGTTCCTTCTTCTCTGTTACCAA     1228
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 TTTAAAAACTTCCATTTTCGTTTTCTTATTTGCATCGGTTCCTTCTTCTCTGTTACCAA     1199

Qy       1229 AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT     1288
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT     1259

Qy       1289 TTAAAAA     1295
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Db       1260 TTAAAAA     1266
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RESULT 13
US-10-225-068-137
; Sequence 137, Application US/10225068
; Publication No. US20050120408A9
; GENERAL INFORMATION:
;   APPLICANT: Mendel Biotechnology, Inc.
;   APPLICANT: Reuber, T. Lynne
;   APPLICANT: Riechmann, Jose Luis
;   APPLICANT: Heard, Jacqueline E.
;   APPLICANT: Jiang, Cai-Zhong
;   APPLICANT: Adam, Luc J.
;   APPLICANT: Dubell, Arnold T.
;   APPLICANT: Ratcliffe, Oliver
;   APPLICANT: Pineda, Omaira
;   APPLICANT: Yu, Guo-Liang
;   APPLICANT: Broun, Pierre E.
;   TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
;   TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
;   FILE REFERENCE: 51444202040
;   CURRENT APPLICATION NUMBER: US/10/225,068
;   CURRENT FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: 60/310,847
;   PRIOR FILING DATE: 2001-08-09
;   PRIOR APPLICATION NUMBER: 60/336,049
;   PRIOR FILING DATE: 2001-11-19
;   PRIOR APPLICATION NUMBER: 60/338,692
;   PRIOR FILING DATE: 2001-12-11
;   PRIOR APPLICATION NUMBER: 10/171,468
;   PRIOR FILING DATE: 2002-06-14
;   NUMBER OF SEQ ID NOS: 246
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 137
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1098)
US-10-225-068-137

Query Match   95.9%;   Score 1255;   DB 21;   Length 1281;
Best Local Similarity   99.9%;   Pred. No. 1.3e-281;
Matches 1266;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;

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Qy    29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT  88
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT  60

Qy    89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 148
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGTAGTAACTTATACAGGATGGGAAGCGGA 208
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGCGATAACTCCGGCGAAAAAGTCGTCGTAGTAACTTATACAGGATGGGAAGCGGA 180

Qy   209 TCAAGCGTTGTGTTAGAATTCAGAGAACGGCGTAGGAAGCTGAATCTAGGAAGCTTCCGTCG 268
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTGTTAGAATTCAGAGAACGGCGTAGGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTTCAGATTTACGAG 328
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCGTGTGGCTCGGACAACATTCAACGAAGAAGAAGACGAAGCCCGTCGTGCCTAC 388
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCGCGTGTGGCTCGGACAACATTCAACGAAGAAGAAGACGAAGCCCGTCGTGCCTAC 360

Qy   389 GACGTCGCCGTTCACAGGTTCCGTCGCCCGTGACCGCCGTCACAAATTCAAAGACGTGAAG 448
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGCCGTTCACAGGTTCCGTCGCCCGTGACCGCCGTCACAAATTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGGTCGATTTCTGAATTCTCATTCGAAATCTGAAATCGATGATCGTGATATG 508
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAAGACGAGGTCGATTTCTGAATTCTCATTCGAAATCTGAAATCGATGATCGTGATATG 480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAGTAAACGGCGTCGTAATGGTAAC 568
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCACGACG 628
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCACGACG 600

Qy   629 GGGTTAGATCGGCGGAGGCACTGTTGAGAAAGCGTAACGCCAAGCGACGTGGGAAG 688
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTGGGAAG 660

Qy   689 CTAAACCGGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGAGTGTTGTTGAACTTGAGGACGTTAACGGGGAAAGTGTGGAGG 808
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGAGTGTTGTTGAACTTGAGGACGTTAACGGGGAAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCGAGTTATGTTTTGACTAAAGGTTTCAGTAACGGT 868
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCGAGTTATGTTTTGACTAAAGGTTTCAGTAACGGT 840

Qy   869 TTCGTTAAGGAGGAAGAATCTACGTGCTGTGGTTGACGTTGGTTAGTTTCAGTTAGATCTTAACGGT 928
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGGAAGAATCTACGTGCTGTGGTTGACGTTGGTTAGTTTCAGTTAGATCTTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCGCGGGTCAGATTTAGATGCGGGT 988
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy  1049 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTTGTGTGTGTAGCAAGAAGCAACGC 1108
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTTGTGTGTGTAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTCACGCGCCTCGTAACAACTCTTCTTCTTTTTTTTCTTTTGTGTTTTAATAATT 1168
         |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  1081 ATCTTCACGCGCCTCGTAACAACTCTTCTTCTC-TTTTTTTTGTTTGTGTTTTAATAATT 1139

Qy  1169 TTTAAAACTCCATTTCGTTTCTTATTGCATCGGTTCTTCTTCTTGTTTACCAA 1228
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAACTCCATTTCGTTTCTTATTGCATCGGTTCTTCTTCTTGTTTACCAA 1199

Qy  1229 AGGTTCATGAGTTGTTTTGTTGTTGATTGATGAACTGTAAATTTATTATTAGGATAAATT 1288
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTGTTGTTGATTGATGAACTGTAAATTTTATTATTAGGATAAATT 1259

Qy  1289 TTAAAAA 1295
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Db  1260 TTAAAAA 1266
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RESULT 14
US-10-225-066A-795
; Sequence 795, Application US/10225066A
; Publication No. US20050160493A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 795
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-795

Query Match   95.9%;   Score 1255;   DB 22;   Length 1281;
Best Local Similarity   99.9%;   Pred. No. 1.3e-281;
Matches 1266;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;

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Qy    29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT  88
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT  60

Qy    89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 148
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 120
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Qy    149  CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA  208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA  180

Qy    209  TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTAGAGCTGAATCTAGGAAGCTTCCGTCG  268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTAGAGCTGAATCTAGGAAGCTTCCGTCG  240

Qy    269  TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAG    328
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAG    300

Qy    329  AAACACCAGCGGCCGTGCGTGCTCCGGACATTCAACGCAAGAGACGAAGCCGCTCGTGCCTAC  388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AAACACCAGCGGCCGTGCGTGCTCCGGACATTCAACGCAAGAGACGAAGCCGCTCGTGCCTAC  360

Qy    389  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCCGTCACAAATTTCAAAGACGTGAAG  448
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCCGTCACAAATTTCAAAGACGTGAAG  420

Qy    449  ATGGACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAGATCGTTGATATG  508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  ATGGACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAGATCGTTGATATG  480

Qy    509  TTGAGGAAACATACTTATAACGAAGAGAGTTAGAGCAGAGAAACGGCCGTCGTAATGGTAAC  568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TTGAGGAAACATACTTATAACGAAGAGAGTTAGAGCAGAGAAACGGCCGTCGTAATGGTAAC  540

Qy    569  GGAAACATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGCATGGTGTTTCTACGACG  628
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGAAACATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGCATGGTGTTTCTACGACG  600

Qy    629  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG  688
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG  660

Qy    689  CTAAACCCGTTGGTTATACCGGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT  748
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTAAACCCGTTGGTTATACCGGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT  720

Qy    749  AACGTTTCCGTGAAAAGGAGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  808
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AACGTTTCCGTGAAAAGGAGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  780

Qy    809  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTTGACTAAAAGGTTGGAGCAGG  868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTTGACTAAAAGGTTGGAGCAGG  840

Qy    869  TTCGTTAAGGAGAAGAATCTACCGTGCTGGTGGGTAGTTCAGTTAGTTTCAGTAGATCTAACGGT  928
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTCGTTAAGGAGAAGAATCTACCGTGCTGGTGGGTAGTTCAGTTAGTTTCAGTAGATCTAACGGT  900

Qy    929  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  960

Qy    989  CGGGTTTTGAGATTGTTCGGAGTTCACCGGAGAGTTCACCGGAGTTCAAGAAACGACGTCGTA  1048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CGGGTTTTGAGATTGTTCGGAGTTCACCGGAGAGTTCACCGGAGTTCAAGAAACGACGTCGTA  1020

Qy    1049  GGAAACAAAGAGAGTGAACGATACGATACTGAGATGTGTTGGTCGTGTGTGTAGCAAGAAGCAACGC  1108
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  GGAAACAAAGAGAGTGAACGATACGATACTGAGATGTGTTGGTCGTGTGTGTAGCAAGAAGCAACGC  1080

Qy    1109  ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTGTTTTGTTTTTAATAATT  1168
            |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    1081  ATCTTTCACGCCTCGTAACAACTCTTCTTC--TTTTTTTTTGTTTTTAATAATT  1139

Qy    1169  TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCCGGTTTCTTCTTCTTGTTTACCAA  1228
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140  TTTAAAAACTCCATTTCCATTTTGCATCCGGTTTCTTCTTCTTGTTTACCAA  1199

Qy    1229  AGGGTTCATGAGTTGTTTGTTTGTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT  1288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200  AGGGTTCATGAGTTGTTTGTTTGTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT  1259

Qy    1289  TTAAAAA  1295
            ||||||
Db    1260  TTAAAAA  1266
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RESULT 15
US-09-938-842A-2316
; Sequence 2316, Application US/09938842A
; Patent No. US2002016037841
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2316
;   LENGTH: 1035
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-2316

Query Match   79.1%; Score 1035; DB 9; Length 1035;
Best Local Similarity   100.0%; Pred. No. 1.9e-230;
Matches 1035; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     92  ATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACGTTCCATCGTGAAACCCCG  151
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Db      1  ATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACGTTCCATCGTGAAACCCCG   60

Qy    152  GCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA  211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA  120

Qy    212  AGGGTTGTGTTAGATTCAGAGAACGGCCGTAGAGCTGAATCTAGGAAGCTTCCGTCGTCA  271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AGCGTTGTGTTAGATTCAGAGAACGGCGTAGAGCTGAATCTAGGAAGCTTCCGTCGTCA  180

Qy    272  AAATACAAAGGTGGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAGAAA  331
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  AAATACAAAGGTGGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAGAAA  240

Qy    332  CACCAGCGGCCGTGCGTGGCTCCGGACATTCAACGCGACGCCGCTCGTGCCTACGAC  391
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CACCAGCGGCCGTGCGTGGCTCCGGACATTCAACGCGACGCCGCTCGTGCCTACGAC  300

Qy    392  GTCGCGGTTCACAGGTTCCGTCGCCGTCGTGAATTCTCAATTCGAAATCTGAGATGTTG  451
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  GTCGCGGTTCACAGGTTCCGTCGCCGTCGTGAATTCTCAATTCGAAATCTGAGATGTTG  360

Qy    452  GACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAAATCTGAAATCGTCGTTGATATGTTG  511
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAAATCTGAAATCGTCGTTGATATGTTG  420

Qy    512  AGGAAACATATACCAAGAGTTAGAGCAGAGAGTAAACGGCGTCGTAATGGTAACGGA  571
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AGGAAACATATACCAAGAGTTAGAGCAGAGAGTAAACGGCGTCGTAATGGTAACGGA  480

Qy    572  AACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGG  631
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Db   481 AACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGG 540

Qy   632 TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTA 691
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Db   541 TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTA 600

Qy   692 AACCGTTTGGTTATACCGAAACATCACGCGAGAGAACATTTCCGTTACCGTCAAGTAAC  751
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Qy   752 GTTTCCGTGAAAGGAGTGTTGTTGAACTTGACGACGTTAACGGGAAAGTGTGGAGGTTC  811
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Db   661 GTTTCCGTGAAAGGAGTGTTGTTGAACTTGACGACGTTAACGGGAAAGTGTGGAGGTTC  720

Qy   812 CGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTTC  871
         |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   721 CGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGGTTC 780

Qy   872 GTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAG 931
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Db   781 GTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAG 840

Qy   932 GATCAACAGTTGTACATTGGGTGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGG  991
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Db   841 GATCAACAGTTGTACATTGGGTGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGG  900

Qy   992 GTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTTCGTAGGA 1051
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Db   901 GTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTTCGTAGGA 960

Qy  1052 AACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTAGCAAGAAGCAACGCATC  1111
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Db   961 AACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGCATC 1020

Qy  1112 TTTCACGCCTCGTAA 1126
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Search completed: September 11, 2005, 09:20:56
Job time : 1005.55 secs

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          September 11, 2005, 00:07:40 ; Search time 4991.21 Seconds
                                    (without alignments)
                                 9975.140 Million cell updates/sec

Title:           US-10-632-436A-1
Perfect score:   1308
Sequence:        1 gtatacatatacacacacata.......ttaaaaagggttacttagat 1308

Scoring table:   IDENTITY_NUC.
                 Gapop 10.0 , Gapext 1.0

Searched:        34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:        68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
             1:  gb_est1:*
             2:  gb_est2:*
             3:  gb_htc:*
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             5:  gb_est4:*
             6:  gb_est5:*
             7:  gb_est6:*
             8:  gb_gss1:*
             9:  gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	Query Match %	Length	DB	ID	Description
1	1261.4	96.4	1275	3	CNS0AAHR	BX817019 Arabidops
2	1226.8	93.8	1397	3	CNS0ABBS	BX815799 Arabidops
3	1179.4	90.2	1309	3	CNS0ABRD	BX816625 Arabidops
4	1157.6	88.5	1391	3	CNS0ABP0	BX816249 Arabidops
5	1108.6	84.8	1387	3	CNS09YIT	BX841829 Arabidops
6	670.2	51.3	704	6	BU635864	BU635864 039F02 In
7	612.6	46.8	1048	6	CB686050	CB686050 Bn01b 03b
8	566	43.3	586	6	CB257063	CB257063 47-E01274
9	534	40.8	534	5	AV527557	AV527557 AV527557
10	518.6	39.6	752	5	BU238054	BU238054 Ds01 14g0
11	504	38.5	504	1	AV537025	AV537025 AV537025
c 12	503.8	38.5	546	1	AV439943	AV439943 AV439943
c 13	493.8	37.8	969	8	BZ458719	BZ458719 BONKU85TF
c 14	493.4	37.7	860	9	AJ597800	AJ597800 Arabidops
c 15	478.4	36.6	480	1	AI994740	AI994740 701499474
16	465.4	35.6	467	1	AV519075	AV519075 AV519075
c 17	423.4	32.4	425	1	AV788518	AV788518 AV788518
c 18	409.6	31.3	428	5	BP606510	BP606510 BP606510
19	406.2	31.1	575	7	N37328	N37328 18555 Lambd
c 20	404	30.9	415	8	BZ768017	BZ768017 SALK 1396
c 21	401.8	30.7	440	1	BP620288	BP620288 BP620288
c 22	398.4	30.5	412	1	AV789688	AV789688 AV789688
c 23	395	30.2	418	5	BP608988	BP608988 BP608988
c 24	384	29.4	420	5	BP612748	BP612748 BP612748

c 25	378.8	29.0	428	1	AV800762	AV800762	AV800762 AV800762
c 26	375.2	28.7	464	1	BP609612	BP609612	BP609612 BP609612
c 27	371.8	28.4	1304	3	CNS0ABR3	CNS0ABR3	BX816580 Arabidops
c 28	356	27.2	421	8	BP643459	BP643459	BP643459 BP643459
c 29	346.2	26.5	434	8	BZ288479	BZ288479	BZ288479 SALK_0218
c 30	341	26.1	371	5	BP602903	BP602903	BP602903 BP602903
31	338.4	25.9	345	7	BP561325	BP561325	BP561325 BP561325
32	338	25.8	484	7	T43470	T43470	T43470 6733 Lambda
c 33	296	22.6	825	8	BZ469001	BZ469001	BZ469001 BONIN92TF
34	295	22.6	392	1	AA597821	AA597821	AA597821 29888 Lam
35	294.8	22.5	315	1	AV520986	AV520986	AV520986 AV520986
36	290.6	22.2	450	7	N37218	N37218	N37218 18428 Lambd
37	288.4	22.0	945	3	CNS0ABW6	CNS0ABW6	BX815867 Arabidops
38	277	21.2	277	7	Z37232	Z37232	Z37232 ATTS3975 AC
39	277	21.2	433	5	BP633826	BP633826	BP633826 BP633826
40	274	20.9	769	5	BQ916903	BQ916903	BQ916903 QHB19N11.
41	272.8	20.9	897	7	CK263261	CK263261	CK263261 EST709339
42	270.6	20.7	756	5	BU636754	BU636754	BU636754 011C04 In
c 43	270.4	20.7	429	5	BP605529	BP605529	BP605529 BP605529
44	269.4	20.6	756	5	BQ971511	BQ971511	BQ971511 QHB7E05.y
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                              ALIGNMENTS

RESULT 1
CNS0AAHR
LOCUS       CNS0AAHR                 1275 bp    mRNA     linear   HTC 06-FEB-2004
DEFINITION  Arabidopsis thaliana Full-length cDNA Complete sequence from clone
            GSLTPGH81ZA05 of Hormone Treated Callus of strain col-0 of
            Arabidopsis thaliana (thale cress).
ACCESSION   BX817019
VERSION     BX817019.1  GI:4247000l
KEYWORDS    HTC; GSLT_cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1275)
AUTHORS     Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
            Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
            Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE       Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
            A Combined Approach to Evaluate and Improve Arabidopsis Genome
            Annotation
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 1275)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT     The sequences are based on single pass reads.
            Life Technologies (a division of Invitrogen) members carried out
            full-length librairies construction : Temple G.
            Genoscope members carried out sequencing and annotation : Castelli
            V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
            Schachter V., Weissenbach J., Salanoubat M.
            URGV INRA : Clepet C., Caboche M.
            Annotation is based on the June 2003 version of the Arabidopsis
            genome released by MIPS (Munich Information center for Protein
            Sequences). 5 prime and 3 prime are assembled with Phrap.
            http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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ORIGIN

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Best Local Similarity 99.8%;  Pred. No. 3.5e-283;
Matches 1273;  Conservative 0;  Mismatches 1;  Indels 1;  Gaps 1;

Qy   34 CACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAACACAGATTAAAT 93
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    1 CACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGATTAAAT 60

Qy   94 GGAATCGAGTAGCGTTGATGAGAGTACTACACAAGTACACAGGTTCCATCTGTGAAACCCCGGC 153
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGAATCGAGTAGCGTTGATGAGAGTACTACACAAGTACACAGGTTCCATCTGTGAAACCCCGGC 120

Qy  154 GATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCAAG 213
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCAAG 180

Qy  214 CGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA 273
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA 240

Qy  274 ATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAGAGAACA 333
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Qy  334 CCAGCGCGTGGCTCGGGACATTCAACGAAGACGAAGCCGCTCGTGCCTCCTACGACGT 393
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Qy  394 CGCGGTTCACAGGTTCCGTGACGCCGTCACAAATTTCAAAGACGTGAAGATGGA 453
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Qy  454 CGAAGACGAGGTCGATTCTTGGAATTCATTCGAAATCTGAGATCGTTGATATGTTGAG 513
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Qy  514 GAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGAAA 573
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Qy  574 CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGGTT 633
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Db  541 CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGGTT 600

Qy  634 TAGATCGGCGGAGGCACTGTTTGAGAAGCGTAACGCCAAGCGACGTTGGGAAGCTAAA 693
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Db  601 TAGATCGGCGGAGGCACTGTTTGAGAAGCGTAACGCCAAGCGACGTTGGGAAGCTAAA 660

Qy  694 CCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGTAACGT 753
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Db  661 CCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGTAACGT 720

Qy  754 TTCCGTGAAAGGAGTGTGTTGTTGAACTTTGTTGGAAGCGTGTGGAAAGTGTGGAGGTCCG 813
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Db  721 TTCCGTGAAAGGAGTGTGTTGTTGAACTTTGTTGGAAGCGTGTGGAAAGTGTGGAGGTTCCG 780

Qy  814 TTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTTCGT 873
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Qy  874 TAAGGAGAAGAATCTACGTCGTCGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGA 933
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Db  841 TAAGGAGAAGAATCTACGTCGTCGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGA 900

Qy  934 TCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGCGGTCGGGT 993
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Qy 1054 CAAAGAGTGAACGATACGAGATGTATCGTTGGTGGTGTAGCAAGAAGCAACGCCATCTT 1113
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Qy 1114 TCACGCCTCGTA-ACAACTCTTCTTCTTCTTTGTTGTTTAATAATTTTA 1172
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Qy 1173 AAAACTCCATTTTCGTTTTCTTATTGGCATCGGTTCTTCTTCCTTGTTTACCAAAGGT 1232
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RESULT 2
CNSOABBS

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LOCUS       CNSOABBS               1397 bp    mRNA    linear   HTC 06-FEB-2004
DEFINITION  Arabidopsis thaliana Full-length cDNA Complete sequence from clone
            GSLTLS9ZE03 of Adult vegetative tissue of strain col-0 of
            Arabidopsis thaliana (thale cress).
ACCESSION   BX815799
VERSION     BX815799.1  GI:42470960
KEYWORDS    HTC; GSLT cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1397)
AUTHORS     Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
            Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
            Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE       Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
            A Combined Approach to Evaluate and Improve Arabidopsis Genome
            Annotation
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 1397)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The sequences are based on single pass reads.
            Life Technologies (a division of Invitrogen) members carried out
            full-length libraries construction : Temple G.
            Genoscope members carried out sequencing and annotation : Castelli
            V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
            Schachter V., Weissenbach J., Salanoubat M.
            URGV INRA : Clepet C., Caboche M.
            Annotation is based on the June 2003 version of the Arabidopsis
            genome released by MIPS (Munich Information center for Protein
            Sequences). 5 prime and 3 prime are assembled with Phrap.
            http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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ORIGIN

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Best Local Similarity   99.0%;  Pred. No. 4.1e-275;
Matches 1245;  Conservative   0;  Mismatches  12;  Indels   1;  Gaps   1;

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Qy    111  ATGAGAGTACTACAAGTACAGAGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAA  170
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Qy    171  AGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCAAGCGGTTGTGTTAGATTCAG  230
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Db    121  AGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCAAGCGGTTGTGTTAGATTCAG  180

Qy    231  AGAACGGCGTAGAGAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGC  290
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Db    181  AGAACGGCGTAGAGAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGC  240

Qy    291  CACAACCAAAACGGCAGATGGGGAGCTCAGATTTACGAGAAAACACCAGCGCGTGTGGCTCG  350
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Db    241  CACAACCAAAACGGCAGATGGGGAGCTCAGATTTACGAGAAAACACCAGCGCGTGTGGCTCG  300

Qy    351  GGACATTCAACGAAGAAGAGAGCGAGCCGCGTCGTCGTGCCTACGACGTCGCGGTTCACAGGTTCC  410
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Db    301  GGACATTCAACGAAGAAGAGAGCGAGCCGCGTCGTCGTGCCTACGACGTCGCGGTTCACAGGTTCC  360

Qy    411  GTCGCCGTGACGCGCCGTCACAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATT  470
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Qy    471  TCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAAACATACTTATACG  530
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Db    421  TCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAAACATACTTATGACG  480

Qy    531  AAGAGTTAGAGCAGAGTAAACGGCCTCGTAATGGTAACGGAACATGACTAGGACGTTGT  590
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Db    481  AAGAGTTAGAGCAGAGTAAACGGCCTCGTAATGGTAACGGAACATGACTAGGACGTTGT  540

Qy    591  TAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGGTTTAGATCGGCGGAGGCAC  650
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Db    541  TAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGGTTTAGATCGGCGGAGGCAC  600

Qy    651  TGTTTGAGAAAGCCGGTAACGCGTAAACCGTTTGGGAAGCTAAACCGTTGGTTATACCGA  710
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TGTTTGAGAAAGCCGGTAACGCGTAACCGCCGCAAGCTAAACCGTTTGGTTATACCGA  660

Qy    711  AACATCACGCAGAGAGAAACATTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGT  770
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  AACATCACGCAGAGAGAAACATTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGT  720

Qy    771  TGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACA  830
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  TGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACA  780

Qy    831  GTAGTCAGAGTATGTTTGACTAAAGGTTGGACCAGGTTCGTTAAGGAGAAGAATCTAC  890
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GTAGTCAGAGTATGTTTGACTAAAGGTTGGACCAGGTTCGTTAAGGAGAAGAATCTAC  840

Qy    891  GTGCTGGTGACGTGGTTAGTTTCAGTTGTCATTGGATCAAGGTCAACAGTTGTACATTG  950
               ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    841  GTGCTGGTGACGTGGTTAGTTTCAGTTGTCAATGGATCAACCGTCAGAGTCAACAGTTGTACATTG  900

Qy    951  GGTGGAAGTCGAGATCCGGGGTCAGATTTAGATGCGGGGTTTTGAGATTGTTCGGAG  1010
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  GGTGGAAGTCGAGATCCGGGGTCAGATTTAGATGCGGGGTCGGTAGGAACAAAGAGTGAACGATA  1070

Qy   1011  TTAACATTTCACCCGGAGAGTTCAAGAAACGACGACGTCGTAGGAACAAAGAGTGAACGATA  1070
               |||||||||||||||||||||||||||||||||||||||||||||
Db    961  TTAACATTTCACCCGGAGAGTTCAAGAAACAAAAGAGTGAACGATA  1020

Qy   1071  CTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTCACGCGCCTCGTAACAAC  1130
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  CTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTCACGCGCCTCGTAACAAC  1080

Qy   1131  TCTTCTCTTTTTTTCTTTTGTTGTTTAATAATTTTTAAAATCCATTTCGTTT  1190
               |||||||||| ||   |||||||||||||||||||||||||||||||||||
Db   1081  TCTTCTTC-TTCCTTTTCTTTTGTCTTAATAATTCCTTAAAAAATCCATTTCGTTT  1139

Qy   1191  TCTTTATTTGCATCGGTTTCTTCTTCTGTTTACCAAAGGTTCATGAGTTGTTTTTGTT  1250
               ||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   1140  TCTTCATTTGCATCGGTTTCTTCTTCTGTTTACCAAAGGTTCATGAGTTGTCTTTGTT  1199

Qy   1251  GTATTGATGAACTGTAAATTTATTTATAAGGATAAATTTTAAAAAGGGTTACTTAGAT  1308
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200  GTATTGATGAACTGTAAATCTCATTTATAGGATAAAATCTTAAAAAGGGTTACTTAGAT  1257


RESULT 3
CNS0ABRD
LOCUS            CNS0ABRD           1309 bp      mRNA         linear   HTC  06-FEB-2004
DEFINITION       Arabidopsis thaliana Full-length cDNA Complete sequence from clone
                 GSLTPGH59ZE10 of Hormone Treated Callus of strain col-0 of
                 Arabidopsis thaliana (thale cress).
ACCESSION        BX816625
VERSION          BX816625.1  GI:42471700
KEYWORDS         HTC; GSLT_cDNA.
SOURCE           Arabidopsis thaliana (thale cress)
ORGANISM         Arabidopsis thaliana
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE        1  (bases 1 to 1309)
AUTHORS          Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
                 Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
                 Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE            Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
                 A Combined Approach to Evaluate and Improve Arabidopsis Genome
                 Annotation
JOURNAL          Unpublished
REFERENCE        2  (bases 1 to 1309)
AUTHORS          Genoscope.
TITLE            Direct Submission
JOURNAL          Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
                 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                 - Web : www.genoscope.cns.fr)
COMMENT          The sequences are based on single pass reads.
                 Life Technologies (a division of Invitrogen) members carried out
                 full-length librairies construction : Temple G.
                 Genoscope members carried out sequencing and annotation : Castelli
                 V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
                 Schachter V., Weissenbach J., Salanoubat M.
                 URGV INRA : Clepet C., Caboche M.
                 Annotation is based on the June 2003 version of the Arabidopsis
                 genome released by MIPS (Munich Information center for Protein
                 Sequences). 5 prime and 3 prime are assembled with Phrap.
                 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                 length
                 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb/ggb?source=Arabidopsis.
FEATURES             Location/Qualifiers
     source          1..1309
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Col-0"
                     /db_xref="taxon:3702"
                     /clone="GSLTPGH59ZE10"
                     /tissue_type="Hormone Treated Callus"
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gene            /plasmid="pCMVSPORT_6"
                1..1309
                /gene="At1g13260"
ORIGIN

Query Match     90.2%;   Score 1179.4;  DB 3;  Length 1309;
Best Local Similarity   96.2%;  Pred. No. 4.5e-264;
Matches 1232;  Conservative 0;  Mismatches 41;  Indels 8;  Gaps 2;

Qy    36 CAAACACATTCGTTCTTCCATTGTTCAAACCATAAAAAAAAAACACAGATTAAATGG   95
            ||||||||||||||  ||||||||||||| |||||||      ||||||||||||||
Db     1 CAAACACATTCGTTTTCTCCATTGTTCAGACCATAAGGGAAAACACAGATTAAATGG   60

Qy    96 AATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCGTGAAACCCCGGCGA  155
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    61 AATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCGTGAGACCCCGGCGA  120

Qy   156 TAACTCCGGCGAAAAAGTCGTCGTAGTAACTTATACAGGATGGGAAGCGGATCAAGCG  215
            ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   121 TAACTCCGGCGAAAGAGTCGTCGTAGTAACTTATACAGGATGGGAAGCGGATCAAGCG  180

Qy   216 TTGTGTTAGATTCAGAGAACGGCGTAGAGCTAGGAGCTTCCGTCGTCTCAAAAT  275
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTGTGTTAGATTCAGAGAACGGCGTAGAGCTAGGAGCTTCCGTCGTCTCAAAAT  240

Qy   276 ACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAGAAACACC  335
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAGAAACACC  300

Qy   336 AGCGCGTGTGGCTCGGGACACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGACGTCG  395
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Db   301 AGCGCGTGTGGCTCGGGACACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGACGTCG  360

Qy   396 CGGTTCACAGGTTCCGTCGCCGTGACCGCCGTACCGCGTCACAAATTTCAAAGACGTGAAGATGACG  455
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CGGTTCACAGGTTCCGTCGCCGTGACCGCCGTACCGCGTCACAAATTTCAAAGACGTGAAGATGACG  420

Qy   456 AAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGA  515
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGA  480

Qy   516 AACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGAAACA  575
            ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AACATATCTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGAAACA  540

Qy   576 TGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTA  635
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTA  600

Qy   636 GATCGGCCGGAGGCACTCGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACC  695
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GATCGGCCGGAGGCACTCGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACC  660

Qy   696 GTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCGTTACCGTCAAGTAACGTTT  755
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCGTTACCGTCAAGTAACGTTT  720

Qy   756 CCGTGAAAGGAGTGTGTTGAACTTGAGGACGTTAACGGACGAAAGTGTGGAGGTTCCGTT  815
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CCGTGAAAGGAGTGTGTTGAACTTGAGGACGTTAACGGACGAAAGTGTGGAGGTTCCGTT  780

Qy   816 ACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGACGCAGGTTCGTTA  875
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGACGCAGGTTCGTTA  840

Qy   876 AGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGATC  935
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGATC  900

Qy   936 AACAGTTGTACATTGTACGTGGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGGGTT  995
            |||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db   901 AACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGGGTT  960

Qy   996 TGAGATTGTTCGGAGTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTAGGAAACA 1055
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGAGATTGTTCGGAGTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTAGGAAACA 1020

Qy  1056 AAAGAGTGAACGATACTGAGATGTTATCGTTCGTGGTGTGAGCAAGAAGCAACGCCATCTTC 1115
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Db  1021 AAAGAGTGAACGATACTGAGATGTTATCGTTCGTGGTGTGAGCAAGAAGCAACGCCATCTTC 1080

Qy  1116 ACGCCTCGTAACAACTCTCTCTCTTTTTTTTTTCTTTGTGTTTAATAATTTTAAA 1175
            |||||||||||                        |||||||||||    |||||
Db  1081 ACGCCTCGTAACGGGCCTTCTTCTTCTTTTTGTCTTCTTGTTTCTTAATAATCTTTAAA 1140

Qy  1176 ACTCCATTTCGTTCTTA-TTTGCATCGGTTTCTTTCTTCTGTTACCAAAGGTTC 1234
            |||  |||||||||||| |||||||||||  ||||||||||||||||||||||
Db  1141 ACTCGCTTTCGTTTCTTACTTTGCATCGGTGTCTTTCTTCTGTTTACCAAAGGTTC 1200

Qy  1235 ATGAGTTGTTTTGTGTATT------GATGAACGTGAAATTTATTTATACGGATAAAT 1287
            |||  ||| |||||| ||       ||||||||||||||  |||||||||||||||
Db  1201 CTGAGTTCTTTTTGTGTATTTGCATGCGTAATATCTTATTTACTACTGAGGATAAAT 1260

Qy  1288 TTTAAAAGGGTTACTTAGAT 1308
            |||| ||||  |||||||||
Db  1261 TTTCAAAGGCTTACCTAGAT 1281
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RESULT 4
CNS0ABP0
LOCUS       CNS0ABP0              1391 bp    mRNA     linear   HTC  06-FEB-2004
DEFINITION  Arabidopsis thaliana Full-length cDNA Complete sequence from clone
            GSLTPGH37ZC03 of Hormone Treated Callus of strain col-0 of
            Arabidopsis thaliana (thale cress).
ACCESSION   BX816249
VERSION     BX816249.1  GI:42471605
KEYWORDS    HTC; GSLT cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 1391)
  AUTHORS   Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
            Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
            Temple,G., Caboche.M., Weissenbach,J. and Salanoubat,M.
  TITLE     Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
            A Combined Approach to Evaluate and Improve Arabidopsis Genome
            Annotation
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1391)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT     The sequences are based on single pass reads.
            Life Technologies (a division of Invitrogen) members carried out
            full-length librairies construction : Temple G.
            Genoscope members carried out sequencing and annotation : Castelli
            V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
            Schachter V., Weissenbach J., Salanoubat M.
            URGV INRA : Clepet C., Caboche M.
            Annotation is based on the June 2003 version of the Arabidopsis
            genome released by MIPS (Munich Information center for Protein
            Sequences). 5 prime and 3 prime are assembled with Phrap.
            http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
            length
            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES             Location/Qualifiers
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          gene      /plasmid="pCMVSPORT_6"
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ORIGIN

          Query Match        88.5%;   Score 1157.6;  DB 3;   Length 1391;
          Best Local Similarity  96.9%;   Pred. No. 5.5e-259;
          Matches 1246;  Conservative  0;  Mismatches  29;  Indels  11;  Gaps  6;

Qy     34  CACAAACACATTTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAACACAGATTAAAT   93
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CACAAACACATTTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAACACAGATTAAAT   60

Qy     94  GGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCGC  153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCGC  120

Qy    154  GATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGATCAAG   213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGATCAAG   180

Qy    214  CGTTGTGTTAGATTCAGAGAACCGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA  273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CGTTGTGTTAGATTCAGAGAACCGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA  240

Qy    274  ATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTACGAGAAACA     333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTACGAGAAACA     300

Qy    334  CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAACGAAGCCGCTCGTGCCTACGACGT  393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAACGAAGCCGCTCGTGCCTACGACGT  360

Qy    394  CGCGGTTCACAGGTTCCGTCGCCGTGACCGCCCGTCACAAATTTCAAAGACTGAAGATGGA  453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  CGCGGTTCACAGGTTCCGTCGCCGTGACCGCCCGTCACAAATTTCAAAGACTGAAGATGGA  420

Qy    454  CGAAGACGGAGGTCGATTTCTTGAATTCTCATTCTGAAATCTGAGATCGTTGATATGTTGAG  513
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Db    421  CGAAGACGGAGGTCGATTTCTTGAATTCTCATTCTGAAATCTGAGATCGTTGATATGTTGAG  480

Qy    514  GAAACATACTTATAACGAAGAGTTAGAACGAGCAGAGAAACGGCGTGTAATGGTAACGGAAA  573
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Db    481  GAAACATACTTATAACGAAGAGTTAGAACGAGCAGAGAAACGGCGTGTAATGGTAACGGAAA  540

Qy    574  CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTT   633
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Db    541  CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTT   600

Qy    634  TAGATCGGCGGCGGAGCACTGTTTGAGAAAGCGGTAACGCGACGTTGGGAAGCTAAA     693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TAGATCGGCGGCGGAGCACTGTTTGAGAAAGCGGTAACGCGACGTTGGGAAGCTAAA     660

Qy    694  CCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGT  753
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Db    661  CCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGT  720

Qy    754  TTCCGTGAAAGGAGTGTTGTTGTTGAACTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCG  813
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Db    721  TTCCGTGAAAGGAGTGTTGTTGTTGAACTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCG  780

Qy    814  TTACTCGTATTGGAACAGTAGCAGAGTCAGAGTTATGTTTGACTAAAGGTTGAGCAGCAGGTTCGT  873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TTACTCGTATTGGAACAGTAGCAGAGTCAGAGTTATGTTTGACTAAAGGTTGAGCAGCAGGTTCGT  840

Qy    874  TAAGGAGAAGAATCTACGTCGTCGTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGA  933
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Db    841  TAAGGAGAAGAATCTACGTCGTCGTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGA  900

Qy    934  TCAACAGTTGTACATTGGGTGGGAGTCGGAGTCCGGGTCAGATTTAGATGCGGGTCGGGT  993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  TCAACAGTTGTACATTGGGTGGGAGTCGGAGTCCGGGTCAGATTTAGATGCGGGTCGGGT  960
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Qy    994  TTTGAGATTGTTCGGAGTTAACATTTCA-CCGGAGAGTTCAAG-AAACGACGTCGTAGGA  1051
           |||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||
Db    961  TTTGAGATTTTTCGGAGTTTACATTTCACCGGAGAGTTCAAGAAACGACGTCGTAGGA    1020

Qy   1052  ----ACAAAAGAGTGAACGATACTGAGATGTTA--TCGTTGGTGTGTAGCAAGAAG--C  1103
               |||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db   1021  AAACAGAGACAGTGTAACGATAAACTGAGATGTTAATCGTTGGTGTGTAGCAAGAAGCAC  1080

Qy   1104  AACGGCATCTTCACGCCTCG-TAACAACTCCTCCTTCTTTTTTTCTTTTGTTGTTTTA  1162
           |||||||||||||||||||| |||||||||||||||||  ||||  ||||||| |||
Db   1081  ACGGCATTCTTCACGCCTCGCTAACCACCCCCCCTTCTTTAATTTTTCTTTTGTGTATTA  1140

Qy   1163  ATAATTTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCTTCTTCCTTGTT  1222
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   1141  ATAATTTTAAAAACTCCATTTCGTTTCTTCATTTGCATCGGTTCTTCTTCCTTGTT  1200

Qy   1223  TACCAAAGGTCATGAGTTGTTTTTGTTGATTGATGAACTGTAAATTTTATTATAGGA  1282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TACCAAGGTTCATGAGTTGTTTTTGTTGATTGATGAACTGTAAATTTTATTATAGGA  1260

Qy   1283  TAAATTTTAAAAAGGGTTACTTAGAT  1308
           ||||||||||||||||||||||||||
Db   1261  TAAATTTTAAAAAGGGTTACTTAGAT  1286
```

```
RESULT 5
CNS09Y1T
LOCUS       CNS09Y1T                1387 bp    mRNA      linear    HTC  06-FEB-2004
DEFINITION  Arabidopsis thaliana Full-length cDNA Complete sequence from clone
            GSLTLS56ZA09 of Adult vegetative tissue of strain col-0 of
            Arabidopsis thaliana (thale cress).
ACCESSION   BX841829
VERSION     BX841829.1  GI:41454487
KEYWORDS    HTC; GSLT; cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1387)
  AUTHORS   Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
            Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
            Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
  TITLE     Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
            A Combined Approach to Evaluate and Improve Arabidopsis Genome
            Annotation
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1387)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The sequences are based on single pass reads.
            Life Technologies (a division of Invitrogen) members carried out
            full-length librairies construction : Temple G.
            Genoscope members carried out sequencing and annotation : Castelli
            V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
            Schachter V., Weissenbach J., Salanoubat M.
            URGV INRA : Clepet C., Caboche M.
            Annotation is based on the June 2003 version of the Arabidopsis
            genome released by MIPS (Munich Information center for Protein
            Sequences). 5 prime and 3 prime are assembled with Phrap.
            http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
            'length
            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES             Location/Qualifiers
     source          1..1387
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Col-0"
                     /db_xref="taxon:3702"
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                /clone="GSLTLS56ZA09"
                /tissue_type="Adult vegetative tissue"
        gene          /plasmid="pCMVSPORT_6"
                1..1387
                /gene="At1g13260"
ORIGIN

Query Match         84.8%;  Score 1108.6;  DB 3;  Length 1387;
Best Local Similarity  95.2%;  Pred. No. 1.4e-247;
Matches 1176;  Conservative  0;  Mismatches  54;  Indels  5;  Gaps  3;

Qy     1 GTATACATATACACAACATAATTCACAACAACAACAAACACATTTCTGTTTTTCTCCATT 60
           ||||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   128 GTATACATATACACAACATAATTCACAACAACAACACACATTTCTGTTTTTCTCCATT 187
Qy    61 GTTTCAAACCATAAAAAAAAACACAGATTAAATGGAATCGAGTGAGCGTTGATGAGAGTAC 120
           ||||||||| |||| |||||||||||||||||||||||||||||||||||||||||||
Db   188 GTTTCAGACCATTAAGGGGAACACAGATTAAGTGGAATCGAGTGAGCGTTGATGAGAGTAC 247
Qy   121 TACAAGTACAGGTTCATCTGTGAAAC-CCCGGCGATAACTCCGGCGAAAAAGTCGTCGG 179
           |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db   248 TACAAGTACAGGTTCCATCTGTGAAACGCCCGCGATAACTCCGGCGAAAGAGTCGTCGG 307
Qy   180 TAGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTGATTCAGAGAACGGCG 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   308 TAGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCG 367
Qy   240 TAGAAAGCTGAATCTAGGAAGCTTCCGTGTCGTCAAAATACAAAGGTGTGCCACAACCAA 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   368 TAGAAAGCTGAATCTAGGAAGCTTCCGTGTCGTCAAAATACAAAGGTGTGCCACAACCAA 427
Qy   300 ACGGAAGAGTGGGAGCTCAGATTTACAGAAACACCAGCGCGTCGGGACATTCA 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   428 ACGGAAGAGATGGGAGCTCAGATTTACAGAAACACCAGCGCGTCGGGACATTCA 487
Qy   360 ACGAAGAGAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCACAGGTTCCGTCGCCGTG 419
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   488 ACGAAGAGAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCACAGGTTCCGTCGCCGTG 547
Qy   420 ACCCCGTCACAAATTTCAAAGACGTGAAGATGGACGAAGAGAGGTCGATTTCTTGAATT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   548 ACCCCGTCACAAATTTCAAAGACGTGAAGATGGACGAAGAGAGGTCGATTTCTTGAATT 607
Qy   480 CTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAGAAACATACTTATAACGAAGAGTTAG 539
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   608 CTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAGAAACATACTTATAACGAAGAGTTAG 667
Qy   540 AGCAGAGTAAACGGCGTCGTAATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGG 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   668 AGCAGAGTAAACGGCGTCCTAATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGG 727
Qy   600 GGTTGAGTAATGATGGGTTTCTCACGACGGGTTAGATCGGCGGAGGCACTGTTTGAGA 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   728 GGTTGAGTAATGATGGGTTTCTCACGACGGGTTAGATCGGCGGAGGCACTGTTTGAGA 787
Qy   660 AAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGAAACATCACG 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   788 AAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGAAACATCACG 847
Qy   720 CAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTGTTGAACT 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   848 CAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTGTTGAACT 907
Qy   780 TTGAGGACGTTAACGGAAAGTGTGGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGA 839
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   908 TTGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGA 967
Qy   840 GTTATGTTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTGGTG 899
           ||| | ||||||||||||||||||||||||| ||| |||||||||||||||||||||
Db   968 GTTATCTCTTGACTAAAGGTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTGGTG 1027
Qy   900 ACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGT 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1028 ACGTGGTTAGTTCAGTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGT 1087
Qy   960 CGAGATCCGGGTCAGATTTAGATGCGGGTCGGGTTTGAGATGATTGTTCGGAGTTAACATTT 1019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1088 CGAGATCCGGGTCAGATTCAGATGCGGGTCGGGTCTTCGAGATTGTTCGGAGTTAACATTT 1147
Qy  1020 CACCGGAGAGTTCAAGAAACGACGTCGTAGGAAACAAAAGAGTGAACGATACTGAGATGT 1079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1148 CACCGGAGAGTTCAAGAAACGACGTCGTAGGAAACAAAAGAGTGAACGATACTGAGATGT 1207
Qy  1080 TATCGTT--GGTGTGTAGCAAGAAGCAACGCATCTTTCACGCGTCGTAACAACTCTCTT 1137
           ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1208 TATCGTTCGGTAGTGTAGCAAGAACGCAACGCATCTCTCACGCGCCTCGTAACAACTCTCTT 1267
Qy  1138 CTTTTTTTTTCTTTGTTGTT--TTAATAATTTTAAAAACTCCATTTTCGTTTTCTTT 1195
           ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db  1268 CTTTTTTTTCTTTTTGTGTGTCCTAATAATTCTTACAAAACTCCCTCCCCCCCCCTT 1327
Qy  1196 ATTTGCATCGGTTTCTTTCTCTTCGTTTACCAAAG 1230
           ||||||||||||||||||||||||||||||||||
Db  1328 CATCTGCACCGGCTCGTTCCTCTTCGTTACCAAAGG 1362
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RESULT 6
BU635864
LOCUS       BU635864                704 bp    mRNA        linear   EST 23-SEP-2002
DEFINITION  039F02 Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
            sequence.
ACCESSION   BU635864
VERSION     BU635864.1  GI:23303119
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S.
            and Welinder,K.G.
  TITLE     EST sequencing of Erysiphe cichoracearum infected Arabidopsis
            plants
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Karen G. Welinder
            Institut for bioteknologi
            Aalborg Universitet
            Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
            Tel: +45 96358467
            Fax: +45 98141808
            Email: kgw@bio.auc.dk.
FEATURES             Location/Qualifiers
     source          1..704
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /dev_stage="Plant 3 weeks old, three days post infection"
                     /clone_lib="Infected Arabidopsis Leaf"
                     /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
                     library of Arabidopsis and B. cichoracearum infected leaf
                     from three weeks old Arabidopsis plants. Plants were
                     harvested 3 days after infection and mRNA oligo dT
                     selected."
ORIGIN

Query Match         51.3%;  Score 670.4;  DB 5;  Length 704;
Best Local Similarity  99.6%;  Pred. No. 1.9e-145;
Matches 693;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy     1 GTATACATATACACAACATAATTCACAACAACAACAAACACATTTCTGTTTTTCTCCATT 60
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    10 GTATACATATACACAACATAA-TCACAACAATAACACACATTTCTGTTTTCTCCATT 68
Qy    61 GTTTCAAACCATAAAAAAAAACACA-GATTAAATGGAATCGAGTGAGCGTTGATGAGAGTA 119
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FEATURES   Location/Qualifiers
source   1..1048
                  /organism="Brassica napus"
                  /mol_type="mRNA"
                  /cultivar="Westar"
                  /db_xref="taxon:3708"
                  /clone="Bn01b_03b14"
                  /tissue_type="fourth leaf"
                  /dev_stage="3 weeks seedling grown at room temperature"
                  /clone_lib="Bn01b_AAFC_EORC transgenic Brassica napus_ove
                  rexpressing_BNCBF17 constitutively_frost_tolerant"
                  /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
                  Site 2: XhoI; Germinated in soil flats and seedlings grown
                  for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
                  light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
                  collected at 9 am and immediately frozen."

ORIGIN

Query Match   46.8%;   Score 612.6; DB 6; Length 1048;
Best Local Similarity   81.1%;   Pred. No. 5.7e-132;
Matches 828;   Conservative   4;   Mismatches 153;   Indels 36; Gaps   9;

Qy   275 TACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAGAAACAC 334
              ||||: ||||||||||||||||||||||| |||||| ||||||| ||||||||||||
Db   1 TACAAAGGGTCTCCCYTCACCCCGAACGGCGTGGGAGYTCAGATTTACGAGAAGCAC 60

Qy   335 CAGCGGCGTGGGCTCGGCGACATTCAACGAGAGACGAAGCCGCTCGTGCCTACGACGTG 394
              |||||||||||||||||||||||:||||| |||||||||| |||||||||||||||||||
Db   61 CAGCGGCGTGGGYTCGGACTTTCAACGAGACGACGAGGCGCGCGTTCTTACGACGTG 120

Qy   395 GCGGTTCACAGGTTCCGTGCGCCGTGACGCGTCACAAATTCAAA-GACGTGAAGATGGA 453
              ||||||| :|||||| |||||||||||||| ||||||||||||| |||||||||||
Db   121 GCGGTTCACCGGKTTCCGAGGCCGAGACGCGTCACGAACTTCAAAGTGGAGGCTCGA 180

Qy   454 CGAAGACGAGGTCGATTTCTTGAATTCTCGAAATCTGAAATCTGGGATCGTTGATATGTTGAG 513
              ||| ||||||||||||||||||||| |||||||||||||||||| |||||||||||||||||
Db   181 CGACGGAGAGGTCGAGTTTTGAGYTCGCATTCGAAATCTGGGATCGTTGATATCTGAG 240

Qy   514 GAAACATACTTATAACGAAGAGAGAGTTAGAGCGAAGAGAGCTAGACGGCTCGAACGGTAAACGGTCGCAAGAA 573
              |||| ||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   241 GAAGCATACGTATAGCGAAGAGAGAGTTAGAGCGAAGAGAGCAAACCGCACGGCAAACGGTAATGCAAGAA 300

Qy   574 CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGAGTGTTCTACGACGGGGTT 633
                                     ||||
Db   301 CGCGGTTAG----------GTCGACGACGCAAAACGACACGGCGTTTCGACGACGGAGTT 348

Qy   634 TAGATCGGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAGCTAAA 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 TAGATCGGGCGGTGTCTTTGTTTGAGAAAACTGTCACGCCGCTAGCGACGTTGGGAGCTAAA 408

Qy   694 CCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTT---ACCGTCAAGTAA 750
              ||||||||| ||||||||||||||||||||||||||||||| |||||||||||||
Db   409 CCGTTACTCTGATACCGAAACACCACCACGCGGAGAAATATTTTCCGTTGCCGCCGTCGAGTAA 468

Qy   751 CGTTTCCGTGAAAGAGTGTTGTTGAGGACGTTAACGGGAAAGTGTGAGGTT 810
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469 CGTTTCCGTTAAGGAGGTGTTGTTGAACTTGAGGACGTGCGCGGGGAAAGTGTGAGGTT 528

Qy   811 CCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAGGTTCGAGCAGGTT 870
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   529 CCGTTACTCGTATTGGAACAGTAGTCAAAGCTATGTTCTGACAAAAGGTTCGGAGCCGGTT 588

Qy   871 CGTTAAGGAAGAATCTACGTGCTGGTGTGGTTAGTTTCAGTAGATCTAACCGTCA 930
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589 TGTTAAGGAAGAATCTGCGTGCTGGTGTGGTTAGTTTCAGCAGATCCGATGGTCA 648

Qy   931 GGATCAACAGTTGTACATTGGGTGGGAAGTCGAGATCCGGG-TCAGATTTAGTAGCGGGTC 989
              |||||||||||||||||||||||||||||||||||||| | |||||||||| ||||||||
Db   649 GGATCAACAGCTATACATTGGGTGGAAGTCTAGATCCGGGATCGGATGTGGAAAACGGGTC 708

Qy   990 -GGGTTTGAGAGTTGTTCGGGAGTTAACATTTCACCGGAGAGTTCAGAAAACGACGTCGTA 1048
                |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   709 GGGGTTTGAGACTGTTCGGGAGTTCAACGTTTCACCGGCGGGTTCAAGAAAACGACGTCGTA 768

Db   69 GTTTCAAACCATAAAAAAAAAACACAGGATTAAATGAATCGAGTAGCGTTGATGAGAGTA 128
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Qy   120 CTACAAGTACAGGTTCCATCTGTGAAACCCCGGATAACTCCGGCGAAAAAGTCGTCGG 179
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   129 CTACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGG 188

Qy   180 TAGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTTAGATTCAGAGAACGG 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   189 TAGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTTAGATTCAGAGAACGG 248

Qy   240 TAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGCCACAACCAA 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   249 TAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGCCACAACCAA 308

Qy   300 ACGGAAGATGGGGAGCTCAGATTTACGAGAAACACCAGCGGCGTGGGCTCGGGACATTCA 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   309 ACGGAAGATGGGGAGCTCAGATTTACGAGAAACACCAGCGGCGTGGGCTCGGGACATTCA 368

Qy   360 ACGAAGAGACGAAGCCCGTCGTCGTGCCTACGACGTCGCGGTTCACAGGTTCCGTCGCCGTG 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   369 ACGAAGAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCACAGGTTCCGTCGCCGTG 428

Qy   420 ACGCCGTCACAAATTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   429 ACGCCGTCACAAATTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATT 488

Qy   480 CTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGAGTTAG 539
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   489 CTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGAGTTAG 548

Qy   540 AGCAGAGTAAACGGCTCGTCGTAATGCTAACATGACTAGGACGTTGTTAACGTCGG 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   549 AGCAGAGTAAACGGCTCGTCGTAATGCTAACATGACTAGGACGTTGTTAACGTCGG 608

Qy   600 GGTTGAGTAATGATGGTGTTTTCTACGACGGGGTTTAGATCGGGCGGAGGCACTGTTTGAGA 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   609 GGTTGAGTAATGATGGTGTTTTCTACGACGGGGTTTAGATCGGGCGGAGGCACTGTTTGAGA 668

Qy   660 AAGCCGTAACGCCAAGCGACGTTGGGAAGCTAAACC 695
              ||||||||||||||||||||||||||||||||||||
Db   669 AAGCCGTAACGCCCAGCGACGTTGGGAAGCTAAACC 704

RESULT 7
CB686050
LOCUS   CB686050   1048 bp   mRNA   linear   EST 09-APR-2003
DEFINITION   Bn01b_03b14_A
             Bn01b AAFC_EORC transgenic Brassica napus overexpressing BNCBF17 c
             onstitutively_frost_tolerant Brassica napus cDNA clone Bn01b_03b14,
             mRNA sequence.
             1 (bases 1 to 1048)
ACCESSION   CB686050
VERSION   CB686050.1   GI:29689775
KEYWORDS   EST.
SOURCE   Brassica napus (rape)
  ORGANISM   Brassica napus
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 1048)
  AUTHORS   Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
             Chagnon,J., Farah,S., Couroux,P. and Hattori,J.
  TITLE   Expressed Sequence Tags from constitutively frost tolerant
             transgenic Brassica napus overexpressing BNCBF17
  JOURNAL   Unpublished (2002)
COMMENT   Contact: Singh,J.A.
             Eastern Cereal and Oilseed Research Centre
             Agriculture and Agri-food Canada
             KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
             0C6, Canada
             Tel: (613) 759-1662
             Fax: (613) 759-1701
             Email: singhja@agr.gc.ca.

Qy   1049 GGAAACAAAGA--GTGAACGATACTGAGATGTTATCGTTGGTGTGTGTTAGCAAGAAGCAA 1105
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   769 GGGAACAAGAGAGTGGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTTAGCAAGAAGCAA 828

Qy   1106 CGCATCTTTCACGCCTCGTAACAACTCTTCTCTTTTTTTTTTTCTTTCGTTGTTTAATA 1165
          |||||||||||||||||||| ||||| |||| ||| ||||||||| ||||||||||
Db   829 CGCATCTTTCACGCCTTGTAACCACTCCTCT-------TTCTTGAGTTTAATA 875

Qy   1166 ATTTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGGTTTCTTCTTCTTGTTAC 1225
          | |||| ||| ||| ||||||| |||||| ||||||| |||||||||
Db   876 ACTTTTTTAATCCCACTTCCATTCTTTTTCAGTTGCATCAGTTTCTTCTT-AGTAC 934

Qy   1226 CAAAGGTTCATGAGTTGTTTTGTTGTATTGATTGATGAACTGTAAATTTATTTATTAGGATAA 1285
          |||||||||||||||||| ||||| ||||| ||||||| ||||||| ||||| |||||||||
Db   935 CAAAGGTTCATGAGTTG-ATTTATTGTAATGATGAACTGTATATCTGTATATTTATTTATTAGGATCA 993

Qy   1286 A 1286
          |
Db   994 A 994

RESULT 8
CB257063
LOCUS   CB257063   586 bp   mRNA   linear   EST 06-NOV-2003
DEFINITION 47-E012740-027-002-N12-T7R MPIZ-ADIS-027 Arabidopsis thaliana cDNA
            clone MPIZp772N122Q 5-PRIME, mRNA sequence.
ACCESSION   CB257063
VERSION   CB257063.1   GI:32881836
KEYWORDS   EST.
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 586)
  AUTHORS   Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
            Mitchell-Olds,T. and Weisshaar,B.
  TITLE   Large-scale identification and analysis of genome-wide
            single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
  JOURNAL   Genome Res. 13 (6), 1250-1257 (2003)
  MEDLINE   22683290
   PUBMED   12799357
COMMENT   Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 0049221506285l
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 586   Std Error: 0.00
            Plate: 2 row: N column: 12
            Seq primer: T7R; CTAATACGACTCACTATGGGA.
FEATURES   Location/Qualifiers
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                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Ei-2"
                     /db_xref="GABI:593031"
                     /db_xref="taxon:3702"
                     /clone="MPIZp772N122Q"
                     /tissue_type="whole plant"
                     /dev_stage="adult plant, mixed stresses"
                     /lab_host="E. coli TOP10"
                     /clone_lib="MPIZ-ADIS-027"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; cDNA
                     library from Arabidopsis thaliana, accession Eifel-2; ten
                     week old total plants grown under long-day conditions in
                     soil, whole adult plants were treated for 24 hours with
                     different stresses, (1) at 4M-0 C in the dark, (2), at 37
                     Grad C in the dark, (3) lying in the lab after removing
                     from soil, (4) in the greenhouse after wounding leaves
                     with a forceps, (5) in the lab watering with a 150 mM
                     NaCl solution, (6) at 26 M-0C in the light/UV; equal

quantities of stressed plant material were pooled; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
primer sites and orientation:
T7-SalI-CACGCGTCCG-5prime-cDNA-polyA-CC-NotI-SP6; Note:
Sequencing granted in the context of the GABI Arabidopsis
Verbund I: Genetic Diversity, 'Establishment of
high-efficiency SNP-based mutation detection' PI: Bernd
Weisshaar Sequence submission managed by RZPD/GABI-primary
database: http://gabi.rzpd.de. This clone is available
from RZPD; contact RZPD (clone@rzpd.de) for further
information."

ORIGIN

Query Match   43.3%;   Score 566;   DB 6; Length 586;
Best Local Similarity   98.8%;   Pred. No. 3.9e-121;
Matches   581; Conservative   0; Mismatches   5; Indels   2; Gaps   1;

Qy   34 CACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAAACACAGATTAAT 93
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1 CACAAACACATTTCTGTTTTCTCCATTGTTTAAACCA--TAAAAAAACACAGATTAAT 58

Qy   94 GGAATCGAGTAGCGTTGATGAGAGTACTACAGTTCATCTGTGAAACCCCGGC 153
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59 GGAATCGAGTAGCGTTGATGAGAGTACTACAGTTCATCTGTGAAACCCCGGC 118

Qy   154 GATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGAAGCCGGATCAAG 213
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 GATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGAAGCCGGATCAAG 178

Qy   214 CGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA 273
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 CGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA 238

Qy   274 ATACAAAGGTGTGGTGCCACAACCAAACGGAGCATGGGGAGCTCAGATTTACGAGAAACA 333
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 ATACAAAGGTGTGGTGCCACAACCAAACGGAGCATGGGGAGCTCAGATTTACGAGAAACA 298

Qy   334 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGACGT 393
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGACGT 358

Qy   394 CGCGGTTCACAGGTTCCGTCGCCGTGACGACGCCGTCACAAATTCAAAGACGTGAAGATGA 453
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 CGCGGTTCACAGGTTCCGTCGCCGTGACGACGCCGTCACAAATTCAAAGACGTGAAGATGGA 418

Qy   454 CGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAG 513
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   419 CGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAG 478

Qy   514 GAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTGTAATGGTAACGGAAA 573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 GAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTGTAATGGTAACGGAAA 538

Qy   574 CATGACTAGGAGCGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTC 621
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   539 CATGACTAGGAGCGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTC 586

RESULT 9
AV527557
LOCUS   AV527557   534 bp   mRNA   linear   EST 19-FEB-2004
DEFINITION AV527557 Arabidopsis thaliana aboveground organs two to six-week
            old Arabidopsis thaliana cDNA clone AP239g12R 5', mRNA sequence.
ACCESSION   AV527557
VERSION   AV527557.1   GI:867085
KEYWORDS   EST.
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE   1 (bases 1 to 534)
AUTHORS   Asamizu,E., Nakamura,Y., Sato,S., and Tabata,S.
TITLE   A large scale analysis of cDNA in Arabidopsis thaliana: Generation
         of 12,028 non-redundant expressed sequence tags from normalized and
         size-selected cDNA libraries
JOURNAL   DNA Res. 7 (3), 175-180 (2000)
MEDLINE   20363093
PUBMED   10907847
COMMENT   Contact: Erika Asamizu
         The First Laboratory for Plant Gene Research
         Kazusa DNA Research Institute
         Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
         Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES
     source   Location/Qualifiers
                1..534
                /organism="Arabidopsis thaliana"
                /mol_type="mRNA"
                /ecotype="Columbia"
                /db_xref="taxon:3702"
                /clone="AP239g12R"
                /tissue_type="aboveground organs"
                /dev_stage="two to six-week old"
                /clone_lib="Arabidopsis thaliana aboveground organs two to
                six-week old"
                /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                XhoI"

ORIGIN

Query Match   40.8%;   Score 534;   DB 1;   Length 534;
Best Local Similarity   100.0%;   Pred. No. 1.1e-113;
Matches   534;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy     82 CACAGATTAAATGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTCCATCTG 141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACAGATTAAATGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTCCATCTG 60

Qy    142 TGAAACCCCGCGGCGATAACTCGGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGG 201
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGAAACCCCGCGGCGATAACTCGGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGG 120

Qy    202 AAGGCGGATCAAGCGGTTGTGTTAGATTCAGAGAACCGCGTGAGAAGCTGAATCTAGGAAGCT 261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGCGGATCAAGCGGTTGTGTTAGATTCAGAGAACCGCGTGAGAAGCTGAATCTAGGAAGCT 180

Qy    262 TCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGAT 321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGAT 240

Qy    322 TTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCG 381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCG 300

Qy    382 TGCCTACGACGTCGGGTTCACAGGTTCCGTCGCGCTGACGCCGTCACAAATTTCAAAGA 441
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCCTACGACGTCGGGTTCACAGGTTCCGTCGCGCTGACGCCGTCACAAATTTCAAAGA 360

Qy    442 CGTGAAGATGGACGAAGACGAGGTCGATTCTTGAATTCTTGAAATCTGAGATCGT 501
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CGTGAAGATGGACGAAGACGAGGTCGATTCTTGAATTCTTGAAATCTGAGATCGT 420

Qy    502 TGATATGTTGAGGGAAACATGACTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAA 561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGATATGTTGAGGGAAACATGACTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAA 480

Qy    562 TGGTAACGGAAACATGACGTTGTTAACGTCGGGGTTGAGTGAATGATGG 615
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGGTAACGGAAACATGACGTTGTTAACGTCGGGGTTGAGTGAATGATGG 534
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RESULT 10
LOCUS   BU238054   752 bp   mRNA   linear   EST 06-SEP-2002
DEFINITION   Ds01_14g02_A Ds01_AAFC_ECORC_cold_stressed_Flixweed_seedlings

ACCESSION   BU238054
VERSION   BU238054.1   GI:22749879
KEYWORDS   EST.
SOURCE   Descurainia sophia
  ORGANISM   Descurainia sophia
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
         rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.
REFERENCE   1 (bases 1 to 752)
AUTHORS   Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J.,
         Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
TITLE   Expressed Sequence Tags from Cold-Stressed Descurainia sophia
         Seedlings
JOURNAL   Unpublished (2001)
COMMENT   Contact: Singh,J.A.
         Eastern Cereal and Oilseed Research Centre
         Agriculture and Agri-food Canada
         KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
         0C6, Canada
         Tel: (613) 759-1662
         Fax: (613) 759-1701
         Email: singhja@agr.gc.ca.
FEATURES
     source   Location/Qualifiers
                1..752
                /organism="Descurainia sophia"
                /mol_type="mRNA"
                /db_xref="taxon:89411"
                /clone="Ds01_14g02"
                /tissue_type="leaf, stem"
                /dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
                /clone_lib="Ds01_AAFC_ECORC_cold_stressed_Flixweed_seedlin
                gs"
                /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI;
                Site_2: Xho I; Plants were grown for 1 month at 20oC/16
                hrs light/day (average 8 leaves, 1 cm tall, weight
                0.02g/plant). Then they were exposed to 2oC, 12 hrs
                light/day, for 1 week. Library prepared by C. Piche using
                stratagene kit."

ORIGIN

Query Match   39.6%;   Score 518.6;   DB 5;   Length 752;
Best Local Similarity   81.6%;   Pred. No. 4.5e-110;
Matches   621;   Conservative   42;   Mismatches   81;   Indels   17;   Gaps   6;

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Qy    493 TGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACG 552
          |||||||||||||||||| :||: :|:| :||||||||||||||||||||||||||||||
Db      1 TGAGATCGTTGATATGTTGAGGAAACATACTACTWACWACGWGWCTGGAGCAGAGTAAACG 60

Qy    553 GCGTCCGTAATGGTAACGGAAACATGACGACGTTGTTAACGTCGGGGTTGAGTAATGA 612
          |||| |||||||||||||||||||||||||||||||||||
Db     61 GCGTCGTAGCCGTAACGGAAACATGTGAGGACGT------CGTCCGTGTTGAATAACGA 114

Qy    613 TGGTGTTCTACGACGGGGTTAGATCGGCGGAGGCACTGTTTGAGAAAG-CGGTAACGC 671
          |||||||||||||||||||||||||||||||||||||||||:  ||||:|| |||||
Db    115 CGGGCGTTCGACGACGGAGGTTTAGATCGGCGGAGCCTCGTTTGAGAAAGYCGGTTACGC 174

Qy    672 CAAGGCACGTTGGGAAGCTAAACCGTTGGTTATACGAAACATCACGCAGAGAAACATT 731
          |||||||||||||||||||||||||| ||: |:: |||:|||||| |||||||||||:
Db    175 CAAGGCACGTTGGGAAGCTGAACCGTTCGKTTATTCCGAAACACCACCACGCGAGAAACATT 234

Qy    732 TTCCGTTACCGTCAAGTAACGTTTCCGTGAAA-GGAGTGTTGTTGAACTTGAGGACGTT 790
          |||||||||||||||||||||||||||||||| :: | |||||: |||||:||||||||
Db    235 TTCCGTTACCGTCAAGTAATGTTTCCGTTAAACGGAGTGCGYTGAACYYCGGAGGMCGTG 294

Qy    791 AACGGGAAAGTGTGAAGCAGGTTCCGTTACTCGTATTGAACAGTAGCTCAGAGTTATGTTTG 850
          |||||||||::| :|||||||||| :||||||||||||||||||||:::|||: |: |
Db    295 AACGGAAAAGTGTGGAAGCAGGTTCCGTTATYCGTATYCGGAACAGTASYTAAASCCAYGTGTTS 354

Qy    851 ACTAAAGGTTGAGCAGCAGTTCCTTAAGGACGAAGAAGAATCTCACGTGCTGTGGTTAGT 910
          ||||:|:: :||||||||||| :|:|||||||||||||||::|||:||||||||||:::|
Db    355 ACCAAAGGTTGSASCCCSTTCGTTAAGGACGAAGAAGAAYCTAYGTGYTGTGACGTSGTTAGT 414
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Qy   335 CAGCGGCGTGTGGCTCGGGACATTCAACGAGAGACGAGCCGCTCGTGCCTACGACGTC 394
          ||||||||||||||||| ||||||:|||||||||||||||||||||||||||||||||
Db   61 CAGCGGCGTGTGGCTCGGGACACATTCAACGAGAGAAGACGAGCCGCTCGTGCCTACGACGTC 120

Qy   395 GCGGTTCACAGGTTCCGGTCGGTTTGAGATTGTTCGGAGTAACATTTCACCGGAGA 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCGGTTCACAGGTTCCGGTCGGTTTGAGATTGTTCGGAGTAACATTTCACCGGAGA 180

Qy   455 GAAGACAGGAGGTCGATTTCTTGAATTCTCATTCGAAAATCTGAGATCGTTGATATGTTGAGG 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAAGACAGGAGGTCGATTTCTTGAATTCTCATTCGAAAATCTGAGATCGTTGATATGTTGAGG 240

Qy   515 AAACATACTTATAACGAAGAGTTAGACGAGCAGAGTAAACGGCGTCGTAATGGTAACGGAAAC 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAACATACTTATAACGAAGAGTTAGACGAGCAGAGTAAACGGCGTCGTAATGGTAACGGAAAC 300

Qy   575 ATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTT 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTT 360

Qy   635 AGATCGGCGGAGGCACTGTTGGAGAAGCGGTGGGAAGCGTTGGGAAGCTAAAC 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGATCGGCGGAGGCACTGTTGGAGAAGCGGTGGGAAGCGTTGGGAAGCTAAAC 420

Qy   695 CGTTTGGTTATACCGAAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTT 754
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CGTTTGGTTATACCGAAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTT 480

Qy   755 TCCGTGAAAGGAGTGTGTTGTTGAAC 778
          ||||||||||||||||||||||||||
Db   481 TCCGTGAAAGGAGTGTGTTGTTGAAC 504

RESULT 12
AV439943/c
LOCUS   AV439943   546 bp   mRNA   linear   EST 18-FEB-2004
DEFINITION AV439943 Arabidopsis thaliana above-ground organ two to six-week
            old Arabidopsis thaliana cDNA clone APD29e05_f 3', mRNA sequence.
ACCESSION   AV439943
VERSION   AV439943.1 GI:7610293
KEYWORDS   EST.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 546)
AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE   A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
JOURNAL   DNA Res. 7 (3), 175-180 (2000)
MEDLINE   20363093
PUBMED   10907847
COMMENT   Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES   Location/Qualifiers
     source   1..546
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="APD29e05_f"
                     /tissue_type="aboveground organs"
                     /dev_stage="two to six-week old"
                     /clone_lib="Arabidopsis thaliana above-ground organ two to
                     six-week old"
                     /note="Vector: pbluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Qy   911 TTCAGTA-GATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGG-AAGTCGAGATCCG 968
          ||||||| ||||| :||::|||| |||||:||||||:||||||||| ||:|||||||||
Db   415 TTCAGTACGAYCTMCGGSYCAGSATCAACAGTTCTACMTTGGGTGGCAAGTCGAGATCCG 474

Qy   969 GGTCAGATTAGATGCGGGTCGGGTTTGAGATTGTTCGGAGTAACATTTCACCGGAGA 1028
          ||||||||||||| |||||||||||||||||||| ||||| |||||||||||||||
Db   475 GGTCGGACTTGGAAGCGGGTCGGGTTGTTCGGASTCAACATTTCACCGGAGA 534

Qy   1029 GTTCAAGAGAAACGACGTCGTAGGAAACAAAAGAAGTGAACGATACTGAGATGGTATCGTTGG 1088
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   535 GTTCGGAGAAACAGCGTCGTAGGGAACAAGAGAGTGAACGATACTGAGATGTATCGTTGG 594

Qy   1089 TGTGTAGCAAGAGCAACGCAACCATCTTCACGCCCTCGTAACAACTCTTCTCTTCTTTTT 1148
          |||::: |||||||| |||||||||||||||||||||| ||||||||||||||||||
Db   595 TGTGTMSTRAAGAASCAACGCAACCATCTTCCACSCCTCGTAACAACTCCTCTTCTCTTTTT 654

Qy   1149 CTTTTGTTGTTTTAATAATTTTTAAAAACTCCATTTTCGTTTTTCTTTATTTGCATCCGTT 1208
          |||||||||||| ::::||||| |:::| |||| ::::| |:|||||| |||||:|
Db   655 TTCTTTCTAAATCATTTTTTTTT------TCTAATWYCACTDYCGTDDDTWAAAATTGTAT 707

Qy   1209 TCTTTCTTTCTTTGTTTACCAAAGGTTCATGAGTTGTTTTGT 1249
          |||||||||||||||||||||||||||||||||||||||||
Db   708 CGGGTCTTCTDATTTACCAAAGGTTCATGAGTTGTTTTGT 748

RESULT 11
AV537025
LOCUS   AV537025   504 bp   mRNA   linear   EST 20-FEB-2004
DEFINITION AV537025 Arabidopsis thaliana liquid-cultured seedlings Columbia
            Arabidopsis thaliana cDNA clone pAZNII0813R 5', mRNA sequence.
ACCESSION   AV537025
VERSION   AV537025.1 GI:8697308
KEYWORDS   EST.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 504)
AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE   A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
JOURNAL   DNA Res. 7 (3), 175-180 (2000)
MEDLINE   20363093
PUBMED   10907847
COMMENT   Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES   Location/Qualifiers
     source   1..504
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="pAZNII0813R"
                     /tissue_type="liquid-cultured seedlings"
                     /clone_lib="Arabidopsis thaliana liquid-cultured seedlings
                     Columbia"
                     /note="Vector: pbluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Query Match   38.5%; Score 504; DB 1; Length 504;
Best Local Similarity   100.0%; Pred. No. 1.1e-106;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   275 TACAAAGGTGTGTGCCACCAACCAAACGGAAGAATGGGAGCTCAGATTTACGAGAAACAC 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TACAAAGGTGTGTGCCACCAACCAAACGGAAGAATGGGAGCTCAGATTTACGAGAAACAC 60

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Query Match          38.5%;   Score 503.8; DB 1;   Length 546;
Best Local Similarity 97.7%;   Pred. No. 1.2e-106;
Matches  511;  Conservative  0;  Mismatches  12;  Indels  0;  Gaps  0;

Qy   778 CTTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCA 837
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 CTTTGAGTACGTTAACCGGAAAAGTGTGAAGGTTCCGTTACTCGTATTGGAACAGTAGTCA 487

Qy   838 GAGTTATGTTTTGACTAAGGTTGGAGCAGGTTGGAGCAGGTTGGAGCAGGTTCCGTGCTGG 897
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 GAGTTATGTTTTGACTAAGGTTGGAGCAGGTTGGAGCAGGAGAATCTACGTGCTGG 427

Qy   898 TGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAA 957
             |||||||||||||||||||||||||||||||||||||||||||||||
Db   426 TAACGTGGTTAGTTTCAGTAGATGTAACCGTCAGGATCAACAGTTGTACATTGGGTGGAA 367

Qy   958 GTCGAGATCCGGGTCAGATTTAGATGCCGGGTCGGGTTTGAGATTGTTCGGAGTTAACAT 1017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 GTCGAGATCCGGGTCAGATTTAGATGCCGGGTCGGGTTTGAGATTGTTCGGAGTTAACAT 307

Qy  1018 TTCACCGGAGAGTTCAAGAAACGACGTCGTCTAGGAAACAAAGAGTGAACGATACTGAGAT 1077
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 TTCACCGGAGAGTTCAAGAAGCCTCCCGTCGTCTAGGAAACAAAGAGTGAACGATACTGAGAT 247

Qy  1078 GTTATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTTCACGCCTCGTAACAACTCTTCTT 1137
             |||||||||||||||||||||||||||||||||||||||||||||
Db   246 GTTATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTTCACGCCTCGTAACAACTCTTCTT 187

Qy  1138 CTTTTTTTTTTTCTTTTGTTTGTTTTAATAATTTTAAAAACTTCCATTTTCGTTTTCTTTAT 1197
             |||||||||||||||||||||||||||||||||||||||||||||
Db   186 CTGTTTTTTTTTTCTTTTGTTTGTTTTAATAAGTTTTAAAAACTTCCATGTTCGTTTTCTTTAT 127

Qy  1198 TTGCATCGGTTTCTTTTCTTTTCTTTCTTGTTTACCAAAGGTTCATGAGTTGTTTTGTATTGA 1257
             |||||||||||||||||||||||||||||||||||||||||||||
Db   126 ATGCATCGGTTTCTTTTCTTTTCTTTCTTGTTTACCAAAGGTTCATGAGTTGTTTTGTATTGA 67

Qy  1258 TGAACTGTAAATTTTATTTATAGATAAATTTTAAAAAGGGGTT 1300
             |||||||||||||||||||||||||||||||||||||
Db    66 TGAACTGTAAATTTTATTTATAGATAAATTTTAAAAAGGGAT 24
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RESULT 13
BZ458719/c
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LOCUS       BZ458719              969 bp    DNA     linear   GSS 13-DEC-2002
DEFINITION  BONKU85TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONKU85,
            genomic survey sequence.
ACCESSION   BZ458719
VERSION     BZ458719.1  GI:2673949
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BONKU85TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1..969
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BONKU85"
                     /clone_lib="BO_1.6_2_KB_tot"
                     /note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared
                     total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Query Match           37.8%;   Score 493.8; DB 8;   Length 969;
Best Local Similarity 76.6%;   Pred. No. 2.8e-104;
Matches  684;  Conservative  0;  Mismatches 169;  Indels  40;  Gaps  5;

Qy   127 TACAGGTTCCATCTGTGAAACCCGGCCATAACTCCGGCGAAAAAGTCGTCGGTAGGTAA 186
             |||||||   |||||  ||||   ||||||||||||  ||||||||||||||
Db   879 TCCACACTCCGGCTAAGATACACCGCCCGAGACGGCGGAAGTCGTCATCTCCGGCGAG 820

Qy   187 CTTATACAGGATGGGAGCGGGATCAAGGTGTGTTAGATTCAGAGAACGGCGTAGAAGC 246
             ||||||  ||||||||||||||||||||||||||||||||||||
Db   819 TTTATACAGAATGGGAGCGGGTTCAAGGCGTGGTTCTCGATTCCCAGAACGGCGTCGAAGC 760

Qy   247 TGAATCTAGGAAGGTTCCGTCGTCAAAATACAAAGGTGGTGCCACAACCAAACGGAG 306
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   759 AGAATCAAGAAGAAGCTCCCGTCGTCAAAATTCAAAGGCCGTCGTCCCTCAGCCAAACGGAG 700

Qy   307 ATGGGAGCTCAGATTTACGAGAAACACCAGCCGTGTGGCTCGGACATTCAACGAAGA 366
             |||||  ||||||||||||||||||||||||||||||||||||||
Db   699 ATGGGAGCTCAGATATACGAGAAGCACAAGCGCGGTTGCTCGGACATTCAACGAAGA 640

Qy   367 AGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCACAGGTTCGTCGCTGACGCGCGT 426
             ||||||  ||||||||||||||||||||||||||||||||||||||||||
Db   639 AGAAGAAGCGGCGGCGTGTCTACGACGTGCCGCTCACCGGTTCCGCGGGTCTGACGCGCGT 580

Qy   427 CACAAATTTCAAAGACGTGAAGATG------------------GACGAAGACGAGTCGA 468
             ||||||||||| ||||| |||                        |||||||||||||||
Db   579 CACTAATTTCAAACCAGCACGACGTTCCCTAACCGTGAAGGTGAGGTGGACGAAGTAAA 520

Qy   469 TTTCTTGAATTCTCATTCGAAATCTGATATCGTTGATAGTTGAGGAAACATACTTATAA 528
             ||||||||||||||||||||||||||||||||||||||
Db   519 GTTCTTAAACGCACATTCGAAATATGAAATATGAGATCGTTGATATGTTGAGGAAACACACTTACAA 460

Qy   529 CGAGAGTTAGAGCAGAGTAAACGGCTCGTAA---TGGTAACGAACAATGACTAGGAC 585
             ||| |||| ||||  |||||||||||||||     |||||||  ||||||||||||||
Db   459 AGAAGAGTTAGAGCAGCAGAGGGAAACGCAAACGTAACGGTGTGTAACGACACGGAAGAGAC 400

Qy   586 GTTGTTAACGTCGGGTTGAGTAATGATGTGTTTCTACGACGGGGTTTAGATCGGCGGA 645
             ||||| |||                           |||||||  ||||||||||||||
Db   399 TGCTAACGTTACGGTTGTGACGGCGACGTTGGAAGCTAAACCGTTTAAAACCGGCGGA 355

Qy   646 GGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGAAGCTAAACCGTTTGGTTAT 705
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   354 GTGTCTGTTTGAGAAAACGGTAACGCCGAGTGACGTCGGGAAGCTAAACCGTTTAGTGAT 295

Qy   706 ACCGAAACATCACGCAGAGAAACATTTTCCGTACCGTCAA---GTAACGTTTCCGTGAA 762
             ||||||||||||||||||||||||||||||||||||        ||||||||||
Db   294 ACCGAAACACCAAGCCGAGAAACATTTTCCGTTAACGGCGGAAACATGTGGAGCAGGTTCCGTGAG 235

Qy   763 AGGAGTGTGTTGAACTTTGAGGACGTTAACGGCGGAAAGTGTGGAGGTTCCGTTACTCGTA 822
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   234 AGGGACGCTGTTGAATTTCGAAGACGTTAACGGGAAAAGTGTGGAGCAGGTTCCGTTACTCGTA 175

Qy   823 TTGGAACAGTAGTCAGAGTTATGTTTTGACTAAGGTTGGAGCAGGTTCGTTAAGGAGAA 882
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   174 TTGGAACAGTAGTCAAAGCTACGTGTTGACTAAGGTTGGAGCAGGTTCGTTCGTTAAAGAGAA 115

Qy   883 GAATCTACGTGCTGGACGTGGTTAGTTTCAGTAGATCTAACGGTCAACAGTT 942
             |||  |||||||||||||||||||||||||||||||||||||||
Db   114 GAGACTCTGTGCCGGTGATTTGATCAGTTTTAAAAGATCTAACGGTCAGGATCAACAGTT 55

Qy   943 GTACATTGGGTGGAAGT-CGAGATCCGGGTCAGATTTAGATGATCGCGGTT 994
             |||||||||||||||| |||||||||||||||||||||||||||||
Db    54 GTATATTGTGTGGAAGTAACAAAGGCGCGGGGTTGGAACAGGATACGGGCCGGGTT 2
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RESULT 14
AJ597800
LOCUS   AJ597800   860 bp   DNA   linear   GSS 15-JAN-2004
DEFINITION   Arabidopsis thaliana T-DNA flanking sequence, left border, clone
             457A08, genomic survey sequence.
ACCESSION   AJ597800
VERSION   AJ597800.1 GI:37947428
KEYWORDS   GSS; left border; T-DNA flanking sequence.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
             Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
             Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE   T-DNA integration into the Arabidopsis genome depends on sequences
             of pre-insertion sites
JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE   22363535
PUBMED   12446565
REFERENCE   2 (bases 1 to 860)
AUTHORS   Balzergue,S.
TITLE   Direct Submission
JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
             Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT   PCR was performed on DNA from transformants of Arabidopsis thaliana
             plants from INRA (Versailles). The DNA fragment(s) resulting from
             the PCR were directly sequenced from the left or the right border
             to determine the genomic sequence flanking the insertion. T-DNA
             derived sequences were removed. Information to order the
             corresponding mutant line and a link to a database providing a
             graphical display of the insertion site are available at
             http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
             been generated in the framework of the French plant genomics
             program 'Genoplante' (http://www.genoplante.com and
             http://genoplante-info.infobiogen.fr).
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:3702"
                     /clone="457A08"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature   1..860
                     /note="T-DNA flanking sequence
                     left border"
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Best Local Similarity 91.2%; Pred. No. 3.4e-104;
Matches 557; Conservative 0; Mismatches 51; Indels 3; Gaps 3;

Qy   1 GTATACATATACACAACATAATTCACACACAACACACAACACATTTCTGTTTTCTCCATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   253 GTATACATATACACAACATAATTCACACACAACACAACACAACACATTTCTGTTTTCTCCATT 312

Qy   61 GTTTCAAACCATAAAAAAAAACACAGATTAAATGGAATGCAGTCGTTGATGAGAGTAC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 GTTTCAAAGCAT-AAAAAAAACACAGATTAAATGGAATGCAGTCGTTGATGAGAGTAC 371

Qy   121 TACAAGTACAGGTTCCATCTGTGAAACCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   372 TACAAGTACAGGTTCCATCTGTGAAACCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 431

Qy   181 AGGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTTTAGATTCAGAGAACGGCGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   432 AGGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTTTAGATTCAGAGAACGGCGT 491

Qy   241 AGAAGCTGAATCTTAGGAGAGCTTCCGTCGTCAAAATACAAAAGGTGTGTGCCACAACCAAA 300
          |||||||||||||||||||||
Db   309 GGGGAGCTCAGATTACGAGAAAACACCAGCGCCGTGTGGCTCGGGACATTCAACGAAGAAG 368

Db   492 AGAGCTGAATCTTAGGAGAAGCTTCCGTCGTCAAAATACAAAAGGTGTGTGCCACAACCAAA 551

Qy   301 CGGAAGATGGGGAGCTCAGATTACGAGAAAACACCAGCGCGTGTGGCTCGGGACATTCAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   552 CGGAAGATGGGGAGCTCAAATTTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCAA 611

Qy   361 CGAAGAAGACGAAGCCGCTCGTGCCTACGACGTTCGCGACGTTCACAGGTTCGTCGCCGTGA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   612 CGAAGAAGACGAAGCCGCTCGTGCCTACGACGTTCGCGACGTTCACAAGTTCCGTCGCCGTGA 671

Qy   421 CGCCGTCACAAATTCAAAGACGTGAAGACGTGACGAGACGAGGTCGATTTCTTGAATTC 480
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   672 CGCCGGCACAAATTTCAAGACGTGAAAATGGGACGACAGCGACGTCAATTTCTTGAATTC 731

Qy   481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGA 540
          || ||| ||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   732 TTATTCGGAAATTGAAATCGTGGAAATATGTGAGAAACTTCTTTATAAC-AAAAGTTAGA 790

Qy   541 GCAGAGTAAACGGCGTCGTAATGGTAACGGAGAAACATGACTAGGACGTGTTAACGTCGGG 600
          |||||||||||||||||||||||||||||||||| |||||||
Db   791 GCA-AATAAACCGCGCGGTAATGGTACCGGACGAACTAAGACCTTTTAAACGCCCGG 849

Qy   601 GTTGAGTAATG 611
          ||||| |||||
Db   850 GTTGAATAATG 860

RESULT 15
AI994740
LOCUS   AI994740   480 bp   mRNA   linear   EST 08-SEP-1999
DEFINITION   701499474 A. thaliana, Ohio State clone set Arabidopsis thaliana
             cDNA clone 701499474, mRNA sequence.
ACCESSION   AI994740
VERSION   AI994740.1 GI:5841645
KEYWORDS   EST.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 480)
AUTHORS   Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,
             Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P.,
             Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D.,
             Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,
             Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,
             Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and
             Hanson,D.
TITLE   Arabidopsis thaliana Gene Expression MicroArray
JOURNAL   Unpublished (1999)
COMMENT   Contact: David Smoller, Ph.D.
             Genome Systems, Inc., a wholly owned subsidiary of Incyte
             Pharmaceuticals, Inc.
             4633 World Parkway Circle, St. Louis, MO 63134, USA
             Tel: 877-577-2733
             Fax: 314-427-3324
             Email: service@genomesystems.com.
FEATURES   Location/Qualifiers
     source   1..480
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                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /clone="701499474"
                     /clone_lib="A. thaliana, Ohio State clone set"
                     /note="cDNA library was made from selected clones from the
                     Arabidopsis thaliana Ohio State clone set."
ORIGIN
Query Match   36.6%; Score 478.4; DB 1; Length 480;
Best Local Similarity 99.8%; Pred. No. 1e-100;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   309 GGGGAGCTCAGATTACGAGAAAACACCAGCGCCGTGTGGCTCGGGACATTCAACGAAGAAG 368
          ||||||||||||||||||||||||

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Db              |||||||||||||||||||||||||||||||||||||||||||
         1 GGGGAGCTCAGATTTACGAGAAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGAAG   60

Qy       369 ACGAAGCCGCTCGTGCCTACGACGTTCGCGGTTCACAGTTCCGTCGCCGTGACGCCGTCA  428
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ACGAAGCCGCTCGTCGTGCCTACGACGTTCGCGGTTCACAGTTCCGTCGCCGTGACGCCGTCA  120

Qy       429 CAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGA  488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGA  180

Qy       489 AATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTA  548
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 AATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTA  240

Qy       549 AACGGCGTCGTAATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTA  608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AACGGCGTCGTAATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTA  300

Qy       609 ATGATGGTGTTTCTACGACGGGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAA  668
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 ATGATGGTGTTTCTACGACGGGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAA  360

Qy       669 CGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAAC  728
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAAC  420

Qy       729 ATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACG  788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       421 ATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGGCG  480
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